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Human Nucleic Acid Sequences from Prostate Tissue

The invention relates to human nucleic acid sequences -- mRNA, cDNA, genomic sequences -- from normal prostate tissue, which code for gene products or parts thereof and their use.

The invention furthermore relates to polypeptides that can be obtained via the sequences and their use.

One very common type of cancer is prostate cancer, for control of which new therapies are necessary. Previously used therapies that are based on a blocking of hormone effects are very often ineffective after a few years since the tumor becomes independent of the hormone, i.e., it continues to grow and forms metastases without the action of hormones.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

A database which consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue.

ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified which are important for tumor formation and proliferation (see Figure 1).

There is, however, the following problem: Since the EST sequences found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this error possibility can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Therefore overlapping ESTs of the same gene were combined into longer sequences (see Figure 1, Figure 2a and Fig.

3). This lengthening and thus coverage of an essentially larger gene area in each of the respective bases are intended to largely avoid the above described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1 - 2b4.

Nucleic acid sequences Seq. ID No. 2-4, 6-10, 12-14, 16-19, 21, 23, 24, 26-33, 35-37, 39, 41-44, 46, 47, 49, 51-55, 58-64 and Seq. ID No. 217-247 which play a part as candidate genes in prostate cancer have now been found.

Nucleic acid sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 are of special interest.

The invention thus relates to nucleic acid sequences, which code a gene product or a part thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID No. 3, 4, 6-8, 12, 16-35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence which is complementary to the nucleic acid sequences named under a) or b).

The invention furthermore relates to a nucleic acid sequence according to one of the sequences Seq. ID No. 3, 4, 6-8, 12, 16-

19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID No. 2-4, 6-10, 12-14, 16-19, 21, 23, 24, 26-33, 35-37, 39, 41-44, 46, 47, 49, 51-55, 58-64 and 217-247, which are expressed elevated in the normal prostate tissue.

The invention furthermore relates to nucleic acid sequences comprising part of the aforementioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 2500 bp, preferably a length of at least 150 to 2000 bp, especially a length from 400 to 1900 bp.

With the partial sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes and vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs, ϕ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), 2. eukaryotic, such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

A control or regulatory sequence is defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P_R, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The obtainable genes are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments obtainable from use.

The nucleic acid sequences according to the invention can be moved into host cells with suitable vectors, in which as the

heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention furthermore relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

Furthermore, this invention relates to polypeptide partial sequences, so-called ORF (open-reading-frame) peptides according to the sequence protocols Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295.

The invention furthermore relates to polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment and that are coded by the nucleic acids of sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

The invention also relates to phage display proteins, which are directed against a polypeptide or a fragment, and which are coded by the nucleic acids of sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 according to the invention.

The polypeptides of sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 according to the invention can also be used as tools for finding active agents against prostate cancer; this is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 for expression of polypeptides, which can also be used as tools for finding active agents against prostate cancer.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID No. 66-71, 73-75, 82, 83,

90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 as pharmaceutical agents in gene therapy for treatment of prostate cancer, or to produce a pharmaceutical agent for treatment of prostate cancer.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice versions, obtainable from cDNAs of sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences), genomic BAC, PAC and Cosmid libraries are screened and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and Cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and Cosmid clones are sequenced in

order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and Cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 for use as vehicles for gene transfer.

Meanings of technical terms and abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes).

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence.

Contig = A set of DNA sequences which can be combined as a result of very great similarities into one sequence (consensus).

Singleton = A contig that contains only one sequence.

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in different proteins.

N = selectively the nucleotide A, T, G or C.

X = selectively one of the 20 naturally occurring amino acids.

Explanation of the alignment parameters

minimal initial match = minimal initial identity area
maximum pads per read = maximum number of insertions
maximum percent mismatch = maximum deviation in %

Explanation of Figures

Figure 1 shows the systematic gene search in the
 Incyte LifeSeq database.

Figure 2 shows the principle of EST assembling
Figures 2b1-2b4 show the entire principle of EST assembling

Figure 3 shows the in-silico subtraction of gene
 expression in different tissues

Figure 4a shows the determination of tissue-specific
 expression via electronic Northern

Figure 4b shows the electronic Northern

Figure 5 shows the isolation of genomic BAC and PAC
 clones.

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

Example 1

Search for tumor-related candidate genes

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence (see Figures 2a and 2b1-2b4).

The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the normal prostate tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (see Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another).

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated.

All sequences that occurred more than four times in one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

Example 2**Algorithm for identification and lengthening of partial cDNA sequences with altered expression pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

2.1. Electronic Northern Blot

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E.W. and Lipman, D.J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T.L.; Schaeffer, A.A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D.J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W.R. and Lipman, D.J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in different EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blot.

2.1.1

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 10 was found which occurs 4x more heavily in normal prostate tissue than in the corresponding tumor tissue.

The possible function of this gene region relates to human MVF-1.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 10

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
	0.0000	0.0026	0.0000	undef
Bladder	0.0040	0.0022	1.8347	0.5450
Breast	0.0061	0.0052	1.1686	0.8557
Ovary	0.0055	0.0000	undef	0.0000
Endocrine tissue	0.0039	0.0000	undef	0.0000
Gastrointestinal	0.0017	0.0088	0.1935	5.1673
Brain	0.0014	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0065	0.0000	undef
Hepatic	0.0021	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0050	0.0024	2.1069	0.4746
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0030	0.0068	0.4342	2.3033
Kidney	0.0019	0.0000	undef	0.0000
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0095	0.0021	4.4745	0.2235
Prostate	0.0017	0.0071	0.2321	4.3088
Uterus	0.0145			
Breast hyperplasia	0.0000			
Small intestine	0.0149			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lung	0.0111
Kidney	0.0124
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0082
Gastrointestinal	0.0244
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0040
Prostate	0.0128
Sensory organs	0.0000

2.1.2

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 18 was found which occurs 6x more heavily in normal prostate tissue than in the tumor tissue.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 18

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
	0.0279	0.0026	10.9109	0.0917
Bladder	0.0040	0.0022	1.8347	0.5450
Breast	0.0000	0.0026	0.0000	undef
Ovary	0.0018	0.0000	undef	0.0000
Endocrine tissue	0.0116	0.0000	undef	0.0000
Gastrointestinal	0.0042	0.0033	1.2902	0.7751
Brain	0.0014	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0065	0.0000	undef
Hepatic	0.0021	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0037	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0034	0.0000	undef	0.0000
Muscle-skeleton	0.0089	0.0000	undef	0.0000
Kidney	0.0019	0.0055	0.3428	2.9168
Pancreas	0.0060	0.0000	undef	0.0000
Penis	0.0119	0.0021	5.5932	0.1788
Prostate	0.0033	0.0071	0.4642	2.1544
Uterus	0.0000			
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

FETUS % freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lung	0.0000
Kidney	0.0000
Prostate	0.0124
Sensory organs	0.0000
	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0272
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lung	0.0082
Nerves	0.0020
Prostate	0.0192
Sensory organs	0.0000

2.1.3

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 24 was found which occurs 5x more heavily in normal prostate tissue than in the tumor tissue.

The possible function of this gene area relates to the counterpart of an unknown gene yeast chromosome XVI.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 24

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0000	0.0153	0.0000	undef
Breast	0.0120	0.0131	0.9174	1.0901
Ovary	0.0091	0.0208	0.4382	2.2819
Endocrine tissue	0.0146	0.0191	0.7655	1.3064
Gastrointestinal	0.0233	0.0143	1.6285	0.6141
Brain	0.0034	0.0077	0.4423	2.2607
Hematopoietic	0.0056	0.0000	undef	0.0000
Skin	0.0149	0.0847	0.1762	5.6754
Hepatic	0.0000	0.0518	0.0000	undef
Heart	0.0095	0.0275	0.3468	2.8832
Testicles	0.0061	0.0234	0.2612	3.8288
Lung	0.0100	0.0165	0.6020	1.6612
Stomach-esophagus	0.0097	0.0153	0.6300	1.5874
Muscle-skeleton	0.0051	0.0180	0.2855	3.5025
Kidney	0.0059	0.0000	undef	0.0000
Pancreas	0.0038	0.0221	0.1714	5.8337
Penis	0.0000	0.0267	0.0000	undef
Prostate	0.0214	0.0043	5.0338	0.1967
Uterus	0.0116	0.0142	0.8123	1.2311
Breast hyperplasia	0.0182			
Small intestine	0.0093			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0061			

FETUS
% freq.

Development	0.0307
Gastrointestinal	0.0123
Brain	0.0125
Hematopoietic	0.0119
Heart-blood vessels	0.0082
Lung	0.0000
Kidney	0.0062
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0068
Endocrine tissue	0.0245
Fetal	0.0041
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0032
Testicles	0.0000
Lung	0.0000
Nerves	0.0010
Prostate	0.0000
Sensory organs	0.0000

2.1.4

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 30 was found which occurs 4x more heavily in normal prostate tissue than in the tumor tissue.

The possible function of this gene area relates to the counterpart of a gene of thaliana of *Caenorhabditis elegans*.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 30

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0040	0.0022	1.8347	0.5450
Ovary	0.0152	0.0026	5.8431	0.1711
Endocrine tissue	0.0000	0.0054	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0025	0.0044	0.5806	1.7224
Hematopoietic	0.0056	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0025	0.0024	1.0534	0.9493
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0095	0.0021	4.4745	0.2235
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0031			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0092
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lung	0.0000
Kidney	0.0000
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0000
Endocrine tissue	0.0245
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0030
Sensory organs	0.0192
	0.0000

2.1.5

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 43 was found which occurs 6x more heavily in normal prostate tissue than in the tumor tissue.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 43

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0120	0.0044	2.7521	0.3634
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0018	0.0027	0.6698	1.4930
Gastrointestinal	0.0058	0.0048	1.2214	0.8187
Brain	0.0051	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0122	0.0000	undef	0.0000
Lung	0.0012	0.0024	0.5267	1.8986
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0059	0.0058	0.8683	1.1517
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0119	0.0021	5.5932	0.1788
Uterus	0.0050	0.0000	undef	0.0000
Breast hyperplasia	0.0145			
Small intestine	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0035			
FETUS % freq.				
Development	0.0000			
Gastrointestinal	0.0031			
Brain	0.0000			
Hematopoietic	0.0039			
Heart-blood vessels	0.0000			
Lung	0.0037			
Kidney	0.0062			
Prostate	0.0000			
Sensory organs	0.0000			

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0065
Testicles	0.0078
Lung	0.0000
Nerves	0.0050
Prostate	0.0000
Sensory organs	0.0000

2.1.5

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 59 was found which occurs 5x more heavily in normal prostate tissue than in the tumor tissue.

The result is as follows:

Electronic Northern Blot for Seq. ID No.: 59

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0093	0.0051	1.8185	0.5499
Breast	0.0067	0.0022	3.0579	0.3270
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0091	0.0027	3.3489	0.2986
Gastrointestinal	0.0058	0.0000	undef	0.0000
Brain	0.0068	0.0088	0.7741	1.2918
Hematopoietic	0.0056	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0050	0.0000	undef	0.0000
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0183	0.0117	1.5671	0.6381
Lung	0.0062	0.0000	undef	0.0000
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0154	0.0180	0.8565	1.1675
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0057	0.0166	0.3428	2.9168
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0333	0.0064	5.2203	0.1916
Uterus	0.0132	0.0000	undef	0.0000
Breast hyperplasia	0.0145			
Small intestine	0.0125			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0131			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0123
Lung	0.0148
Kidney	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Ovary-uterus	0.0068
Endocrine tissue	0.0245
Fetal	0.0082
Gastrointestinal	
Hematopoietic	0.0244
Skin-muscle	0.0000
Testicles	0.0259
Lung	0.0000
Nerves	0.0000
Prostate	0.0010
Sensory organs	0.0064
	0.0000

In an analogous procedure, the following Northern blots were also found:

Electronic Northern Blot for Seq. ID No.: 2

	NORMAL % freq.	TUMOR % freq.	Ratios N/T T/N	
Bladder	0.0418	0.0383	1.0911	0.9165
Breast	0.0267	0.0218	1.2232	0.8176
Ovary	0.0122	0.0052	2.3372	0.4279
Endocrine tissue	0.0055	0.0109	0.5023	1.9907
Gastrointestinal	0.0136	0.0048	2.8499	0.3509
Brain	0.0093	0.0142	0.6550	1.5267
Hematopoietic	0.0224	0.0000	undef	0.0000
Skin	0.0099	0.0847	0.1175	8.5131
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0180	0.0000	undef	0.0000
Testicles	0.0061	0.0234	0.2612	3.8288
Lung	0.0137	0.0071	1.9313	0.5178
Stomach-esophagus	0.0193	0.0230	0.8399	1.1905
Muscle-skeleton	0.0103	0.0060	1.7130	0.5838
Kidney	0.0089	0.0000	undef	0.0000
Pancreas	0.0076	0.0110	0.6857	1.4584
Penis	0.0269	0.0000	undef	0.0000
Prostate	0.0143	0.0021	6.7118	0.1490
Uterus	0.0463	0.0356	1.2997	0.7694
Breast hyperplasia	0.0109			
Small intestine	0.0312			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0267			
Sensory organs	0.0353			
White blood cells	0.0174			

FETUS % freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0125
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lung	0.0370
Kidney	0.0124
Prostate	0.0748
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.1156
Ovary-uterus	0.0525
Endocrine tissue	0.0245
Fetal	0.0082
Gastrointestinal	0.0366
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles	0.0000
Lung	0.0082
Nerves	0.0151
Prostate	0.0385
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 3

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0093	0.0022	4.2811	0.2336
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0109	0.0027	4.0187	0.2488
Gastrointestinal	0.0039	0.0000	undef	0.0000
Brain	0.0068	0.0077	0.8847	1.1303
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0099	0.0065	1.5303	0.6535
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0061	0.0000	undef	0.0000
Lungs	0.0050	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidneys	0.0030	0.0137	0.2171	4.6066
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0095	0.0043	2.2373	0.4470
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0059			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0082
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0068
Endocrine tissue	0.0245
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0162
Testicles	0.0156
Lungs	0.0000
Nerves	0.0030
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 4

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0051	1.8185 0.5499
Breast	0.0053	0.0022	2.4463 0.4088
Ovary	0.0030	0.0026	1.1686 0.8557
Endocrine tissue	0.0055	0.0000	undef 0.0000
Gastrointestinal	0.0019	0.0000	undef 0.0000
Brain	0.0008	0.0055	0.1548 6.4591
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0000	0.0065	0.0000 undef
Heart	0.0053	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lungs	0.0050	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0051	0.0000	undef 0.0000
Kidneys	0.0089	0.0000	undef 0.0000
Pancreas	0.0038	0.0055	0.6857 1.4584
Penis	0.0000	0.0000	undef undef
Prostate	0.0048	0.0021	2.2373 0.4470
Uterus	0.0116	0.0000	undef 0.0000
Breast hyperplasia	0.0000		
Small intestine	0.0000		
Prostatic hyperplasia	0.0178		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

	0.0000
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0062
Kidneys	0.0000
Prostate	0.0279
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0134
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0518
Testicles	0.0000
Lungs	0.0000
Nerves	0.0060
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 6

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0046	0.0026	1.8185 0.5499
Breast	0.0053	0.0022	2.4463 0.4088
Ovary	0.0030	0.0026	1.1686 0.8557
Endocrine tissue	0.0055	0.0109	0.5023 1.9907
Gastrointestinal	0.0136	0.0048	2.8499 0.3509
Brain	0.0068	0.0066	1.0321 0.9689
Hematopoietic	0.0098	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0050	0.0129	0.3826 2.6139
Heart	0.0074	0.0000	undef 0.0000
Testicles	0.0061	0.0117	0.5224 1.9144
Lungs	0.0100	0.0024	4.2137 0.2373
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0051	0.0000	undef 0.0000
Kidneys	0.0059	0.0068	0.8683 1.1517
Pancreas	0.0170	0.0055	3.0855 0.3241
Penis	0.0030	0.0000	undef 0.0000
Prostate	0.0095	0.0021	4.4745 0.2235
Uterus	0.0017	0.0142	0.1160 8.6176
Breast hyperplasia	0.0036		
Small intestine	0.0062		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0096		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0079
Heart-blood vessels	0.0123
Lungs	0.0037
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Ovary-uterus	0.0205
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0130
Testicles	0.0234
Lungs	0.0000
Nerves	0.0070
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 7

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0077	1.2123 0.8249
Breast	0.0107	0.0131	0.8154 1.2263
Ovary	0.0030	0.0078	0.3895 2.5671
Endocrine tissue	0.0146	0.0000	undef 0.0000
Gastrointestinal	0.0097	0.0143	0.6786 1.4737
Brain	0.0170	0.0088	1.9353 0.5167
Hematopoietic	0.0098	0.0378	0.2587 3.8650
Skin	0.0298	0.0000	undef 0.0000
Hepatic	0.0000	0.0194	0.0000 undef
Heart	0.0159	0.0137	1.1561 0.8650
Testicles	0.0061	0.0000	undef 0.0000
Lungs	0.0112	0.0142	0.7901 1.2657
Stomach-esophagus	0.0000	0.0153	0.0000 undef
Muscle-skeleton	0.0051	0.0060	0.8565 1.1675
Kidneys	0.0178	0.0068	2.6050 0.3839
Pancreas	0.0038	0.0387	0.0980 10.2089
Penis	0.0120	0.0000	undef 0.0000
Prostate	0.0095	0.0021	4.4745 0.2235
Uterus	0.0099	0.0000	undef 0.0000
Breast hyperplasia	0.0109		
Small intestine	0.0125		
Prostatic hyperplasia	0.0119		
Seminal vesicles	0.0356		
Sensory organs	0.0000		
White blood cells	0.0096		

FETUS
% freq.

	0.0000
Development	0.0031
Gastrointestinal	0.0188
Brain	0.0039
Hematopoietic	0.0000
Heart-blood vessels	0.0148
Lungs	0.0185
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0068
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0244
Hematopoietic	0.0057
Skin-muscle	0.0162
Testicles	0.0078
Lungs	0.0492
Nerves	0.0161
Prostate	0.0192
Sensory organs	0.0077

Electronic Northern Blot for SEQ. ID. NO: 8

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0120	0.0109	1.1008	0.9084
Breast	0.0061	0.0052	1.1686	0.8557
Ovary	0.0146	0.0136	1.0716	0.9331
Endocrine tissue	0.0155	0.0143	1.0857	0.9211
Gastrointestinal	0.0136	0.0142	0.9527	1.0496
Brain	0.0042	0.0000	undef	0.0000
Hematopoietic	0.0149	0.0000	undef	0.0000
Skin	0.0050	0.0065	0.7651	1.3069
Hepatic	0.0170	0.0000	undef	0.0000
Heart	0.0000	0.0117	0.0000	undef
Testicles	0.0112	0.0095	1.1851	0.8438
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0051	0.0060	0.8565	1.1675
Muscle-skeleton	0.0119	0.0068	1.7366	0.5758
Kidneys	0.0038	0.0000	undef	0.0000
Pancreas	0.0120	0.0000	undef	0.0000
Penis	0.0143	0.0064	2.2373	0.4470
Prostate	0.0033	0.0000	undef	0.0000
Uterus	0.0036			
Breast hyperplasia	0.0000			
Small intestine	0.0030			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0000			
Sensory organs	0.0113			
White blood cells				

FETUS
% freq.

	0.0000
Development	0.0123
Gastrointestinal	0.0063
Brain	0.0000
Hematopoietic	0.0164
Heart-blood vessels	0.0037
Lungs	0.0185
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0070
Gastrointestinal	0.0122
Hematopoietic	0.0114
Skin-muscle	0.0291
Testicles	0.0156
Lungs	0.0082
Nerves	0.0191
Prostate	0.0064
Sensory organs	0.0155

Electronic Northern Blot for SEQ. ID. NO: 9

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0232	0.0026	9.0924 0.1100
Bladder	0.0187	0.0087	2.1405 0.4672
Breast	0.0122	0.0156	0.7791 1.2836
Ovary	0.0219	0.0136	1.6075 0.6221
Endocrine tissue	0.0116	0.0190	0.6107 1.6375
Gastrointestinal	0.0119	0.0142	0.8337 1.1995
Brain	0.0126	0.0000	undef 0.0000
Hematopoietic	0.0199	0.0000	undef 0.0000
Skin	0.0099	0.0000	undef 0.0000
Hepatic	0.0159	0.0137	1.1561 0.8650
Heart	0.0122	0.0351	0.3482 2.8716
Testicles	0.0187	0.0378	0.4938 2.0251
Lungs	0.0097	0.0307	0.3150 3.1748
Stomach-esophagus	0.0103	0.0120	0.8565 1.1675
Muscle-skeleton	0.0238	0.0000	undef 0.0000
Kidneys	0.0076	0.0055	1.3713 0.7292
Pancreas	0.0180	0.0267	0.6739 1.4840
Penis	0.0214	0.0085	2.5169 0.3973
Prostate	0.0132	0.0285	0.4642 2.1544
Uterus	0.0291		
Breast hyperplasia	0.0156		
Small intestine	0.0268		
Prostatic hyperplasia	0.0356		
Seminal vesicles	0.0235		
Sensory organs	0.0131		
White blood cells			

FETUS
% freq.

	0.0307
Development	0.0247
Gastrointestinal	0.0063
Brain	0.0236
Hematopoietic	0.0286
Heart-blood vessels	0.0111
Lungs	0.0371
Kidneys	0.0997
Prostate	0.0279
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	0.0068
Breast	0.0023
Ovary-uterus	0.0000
Endocrine tissue	0.0064
Fetal	0.0122
Gastrointestinal	0.0057
Hematopoietic	0.0065
Skin-muscle	0.0312
Testicles	0.0082
Lungs	0.0050
Nerves	0.0064
Prostate	0.0000
Sensory organs	

Electronic Northern Blot for SEQ. ID. NO: 12

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0027	0.0044	0.6116	1.6351
Breast	0.0000	0.0156	0.0000	undef
Ovary	0.0018	0.0027	0.6698	1.4930
Endocrine tissue	0.0078	0.0000	undef	0.0000
Gastrointestinal	0.0034	0.0011	3.0964	0.3230
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0050	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0053	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0112	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0034	0.0060	0.5710	1.7513
Muscle-skeleton	0.0089	0.0068	1.3025	0.7678
Kidneys	0.0076	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0048	0.0021	2.2373	0.4470
Prostate	0.0017	0.0000	undef	0.0000
Uterus	0.0036			
Breast hyperplasia	0.0156			
Small intestine	0.0089			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0052			

FETUS
% freq.

	0.0000
Development	0.0031
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0074
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0140
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	0.0000
Breast	0.0046
Ovary-uterus	0.0000
Endocrine tissue	0.0047
Fetal	0.0000
Gastrointestinal	0.0057
Hematopoietic	0.0130
Skin-muscle	0.0156
Testicles	0.0000
Lungs	0.0030
Nerves	0.0064
Prostate	0.0000
Sensory organs	

Electronic Northern Blot for SEQ. ID. NO: 13

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0128	0.0000	undef
Bladder	0.0120	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Ovary	0.0036	0.0000	undef	0.0000
Endocrine tissue	0.0039	0.0000	undef	0.0000
Gastrointestinal	0.0017	0.0066	0.2580	3.8754
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0050	0.0000	undef	0.0000
Skin	0.0000	0.0129	0.0000	undef
Hepatic	0.0074	0.0000	undef	0.0000
Heart	0.0000	0.0117	0.0000	undef
Testicles	0.0087	0.0071	1.2290	0.8137
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0086	0.0060	1.4275	0.7005
Muscle-skeleton	0.0000	0.0137	0.0000	undef
Kidneys	0.0038	0.0000	undef	0.0000
Pancreas	0.0150	0.0000	undef	0.0000
Penis	0.0048	0.0021	2.2373	0.4470
Prostate	0.0066	0.0071	0.9283	1.0772
Uterus	0.0218			
Breast hyperplasia	0.0062			
Small intestine	0.0030			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0353			
Sensory organs	0.0000			
White blood cells				

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0060
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 14

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0051	0.9092	1.0998
Breast	0.0027	0.0000	undef	0.0000
Ovary	0.0091	0.0000	undef	0.0000
Endocrine tissue	0.0018	0.0000	undef	0.0000
Gastrointestinal	0.0039	0.0000	undef	0.0000
Brain	0.0025	0.0022	1.1612	0.8612
Hematopoietic	0.0014	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0137	0.1541	6.4872
Testicles	0.0000	0.0117	0.0000	undef
Lungs	0.0012	0.0024	0.5267	1.8986
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0157	0.0000	undef	0.0000
Uterus	0.0017	0.0071	0.2321	4.3088
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0052			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0078
Nerves	0.0000
Prostate	0.0020
Sensory organs	0.0192
	0.0000

Electronic Northern Blot for SEQ. ID. NO: 16

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0000	undef	0.0000
Breast	0.0120	0.0022	5.5042	0.1817
Breast	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0019	0.0048	0.4071	2.4562
Gastrointestinal	0.0085	0.0219	0.3871	2.5836
Brain	0.0014	0.0000	undef	0.0000
Hematopoietic	0.0050	0.0000	undef	0.0000
Skin	0.0000	0.0259	0.0000	undef
Hepatic	0.0032	0.0000	undef	0.0000
Heart	0.0122	0.0000	undef	0.0000
Testicles	0.0037	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0223	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0071	0.0000	undef	0.0000
Uterus	0.0182	0.0000	undef	0.0000
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0267			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0041
Heart-blood vessels	0.0037
Lungs	0.0124
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Ovary-uterus	0.0046
Endocrine tissue	0.0245
Fetal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0050
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 17

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0026	3.6370	0.2750
Breast	0.0053	0.0065	0.8154	1.2263
Ovary	0.0000	0.0104	0.0000	undef
Endocrine tissue	0.0091	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0048	0.4071	2.4562
Brain	0.0017	0.0022	0.7741	1.2918
Hematopoietic	0.0042	0.0378	0.1109	9.0183
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0061	0.0000	undef	0.0000
Lungs	0.0112	0.0071	1.5801	0.6329
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0086	0.0060	1.4275	0.7005
Kidneys	0.0059	0.0068	0.8683	1.1517
Pancreas	0.0057	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0095	0.0043	2.2373	0.4470
Uterus	0.0050	0.0071	0.6963	1.4363
Breast hyperplasia	0.0000			
Small intestine	0.0031			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0089			
Sensory organs	0.0118			
White blood cells	0.0044			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0164
Nerves	0.0010
Prostate	0.0128
Sensory organs	0.0387

Electronic Northern Blot for SEQ. ID. NO: 19

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0128	0.7274	1.3748
Breast	0.0080	0.0065	1.2232	0.8176
Ovary	0.0091	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0039	0.0000	undef	0.0000
Brain	0.0042	0.0044	0.9676	1.0335
Hematopoietic	0.0070	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0032	0.0137	0.2312	4.3248
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0037	0.0118	0.3160	3.1643
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidneys	0.0089	0.0000	undef	0.0000
Pancreas	0.0019	0.0055	0.3428	2.9168
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0119	0.0064	1.8644	0.5364
Uterus	0.0099	0.0000	undef	0.0000
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0178			
Sensory organs	0.0000			
White blood cells	0.0044			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0157
Heart-blood vessels	0.0082
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0192
	0.0155

Electronic Northern Blot for SEQ. ID. NO: 21

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0128	0.3637	2.7495
Breast	0.0013	0.0087	0.1529	6.5404
Ovary	0.0061	0.0104	0.5843	1.7114
Endocrine tissue	0.0128	0.0136	0.9377	1.0664
Gastrointestinal	0.0078	0.0143	0.5428	1.8422
Brain	0.0102	0.0131	0.7741	1.2918
Hematopoietic	0.0042	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0117	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0025	0.0165	0.1505	6.6450
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0120	0.0120	0.9993	1.0007
Kidneys	0.0178	0.0068	2.6050	0.3839
Pancreas	0.0076	0.0110	0.6857	1.4584
Penis	0.0090	0.0267	0.3369	2.9680
Prostate	0.0167	0.0064	2.6101	0.3831
Uterus	0.0066	0.0214	0.3094	3.2316
Breast hyperplasia	0.0000			
Small intestine	0.0093			
Prostatic hyperplasia	0.0208			
Seminal vesicles	0.0267			
Sensory organs	0.0000			
White blood cells	0.0044			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0247
Brain	0.0188
Hematopoietic	0.0079
Heart-blood vessels	0.0245
Lungs	0.0037
Kidneys	0.0247
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0134
Gastrointestinal	0.0000
Hematopoietic	0.0114
Skin-muscle	0.0259
Testicles	0.0000
Lungs	0.0000
Nerves	0.0100
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 23

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0000	undef	0.0000
Breast	0.0013	0.0087	0.1529	6.5404
Ovary	0.0030	0.0078	0.3895	2.5671
Endocrine tissue	0.0036	0.0054	0.6698	1.4930
Gastrointestinal	0.0039	0.0048	0.8143	1.2281
Brain	0.0025	0.0033	0.7741	1.2918
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0025	0.0047	0.5267	1.8986
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0060	0.2855	3.5025
Kidneys	0.0089	0.0068	1.3025	0.7678
Pancreas	0.0095	0.0055	1.7142	0.5834
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0024	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0149			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0123
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0082
Nerves	0.0010
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 26

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0027	0.0044	0.6116	1.6351
Ovary	0.0061	0.0052	1.1686	0.8557
Endocrine tissue	0.0109	0.0027	4.0187	0.2488
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0068	0.0011	6.1928	0.1615
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0122	0.0000	undef	0.0000
Lungs	0.0012	0.0071	0.1756	5.6957
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0060	0.2855	3.5025
Kidneys	0.0030	0.0068	0.4342	2.3033
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0119	0.0000	undef	0.0000
Uterus	0.0033	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0183
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0078
Lungs	0.0000
Nerves	0.0000
Prostate	0.0030
Sensory organs	0.0064
	0.0000

Electronic Northern Blot for SEQ. ID. NO: 27

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0027	0.0022	1.2232	0.8176
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0018	0.0027	0.6698	1.4930
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0025	0.0022	1.1612	0.8612
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lungs	0.0025	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0071	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0192
Sensory organs	0.0077

Electronic Northern Blot for SEQ. ID. NO: 28

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0040	0.0000	undef	0.000
Ovary	0.0030	0.0052	0.5843	1.7114
Endocrine tissue	0.0036	0.0027	1.3396	0.7465
Gastrointestinal	0.0058	0.0048	1.2214	0.8187
Brain	0.0017	0.0022	0.7741	1.2918
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0183	0.0000	undef	0.0000
Lungs	0.0050	0.0024	2.1069	0.4746
Stomach-esophagus	0.0097	0.0077	1.2599	0.7937
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidneys	0.0059	0.0000	undef	0.0000
Pancreas	0.0019	0.0110	0.1714	5.8337
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0119	0.0043	2.7966	0.3576
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0031
Brain	0.0063
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0192
	0.0000

Electronic Northern Blot for SEQ. ID. NO: 29

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0055	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0093	0.0022	4.2576	0.2349
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0050	0.0065	0.7651	1.3069
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0025	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidneys	0.0059	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0048	0.0000	undef	0.0000
Uterus	0.0066	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0031			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0078
Lungs	0.0000
Nerves	0.0141
Prostate	0.0256
Sensory organs	0.0077

Electronic Northern Blot for SEQ. ID. NO: 31

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Ovary	0.0018	0.0000	undef	0.0000
Endocrine tissue	0.0019	0.0048	0.4071	2.4562
Gastrointestinal	0.0000	0.0022	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0024	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0095	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0073			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 32

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0027	0.0022	1.2232	0.8176
Ovary	0.0091	0.0078	1.1686	0.8557
Endocrine tissue	0.0055	0.0136	0.4019	2.4884
Gastrointestinal	0.0019	0.0095	0.2036	4.9124
Brain	0.0076	0.0044	1.7417	0.5741
Hematopoietic	0.0028	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0050	0.0000	undef	0.0000
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0122	0.0000	undef	0.0000
Lungs	0.0012	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0180	0.0952	10.5076
Kidneys	0.0030	0.0068	0.4342	2.3033
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0048	0.0000	undef	0.0000
Uterus	0.0017	0.0142	0.1160	8.6176
Breast hyperplasia	0.0109			
Small intestine	0.0062			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0154
Brain	0.0125
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0128
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0097
Testicles	0.0468
Lungs	0.0082
Nerves	0.0060
Prostate	0.0192
Sensory organs	0.0232

Electronic Northern Blot for SEQ. ID. NO: 33

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0046	0.0026	1.8185 0.5499
Breast	0.0013	0.0022	0.6116 1.6351
Breast	0.0000	0.0026	0.0000 undef
Ovary	0.0055	0.0000	undef 0.0000
Endocrine tissue	0.0019	0.0000	undef 0.0000
Gastrointestinal	0.0042	0.0077	0.5529 1.8085
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0129	0.0000 undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0025	0.0047	0.5267 1.8986
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0030	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0030	0.0000	undef 0.0000
Prostate	0.0071	0.0021	3.3559 0.2980
Uterus	0.0017	0.0000	undef 0.0000
Breast hyperplasia	0.0000		
Small intestine	0.0062		
Prostatic hyperplasia	0.0119		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0017		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 35

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0026	0.0000 undef
Breast	0.0093	0.0065	1.4270 0.7008
Ovary	0.0091	0.0130	0.7012 1.4262
Endocrine tissue	0.0055	0.0027	2.0093 0.4977
Gastrointestinal	0.0039	0.0190	0.2036 4.9124
Brain	0.0008	0.0033	0.2580 3.8754
Hematopoietic	0.0112	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0053	0.0137	0.3854 2.5949
Testicles	0.0000	0.0000	undef undef
Lungs	0.0037	0.0024	1.5801 0.6329
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0017	0.0060	0.2855 3.5025
Kidneys	0.0089	0.0137	0.6512 1.5355
Pancreas	0.0057	0.0000	undef 0.0000
Penis	0.0120	0.0000	undef 0.0000
Prostate	0.0095	0.0021	4.4745 0.2235
Uterus	0.0033	0.0000	undef 0.0000
Breast hyperplasia	0.0000		
Small intestine	0.0093		
Prostatic hyperplasia	0.0030		
Seminal vesicles	0.0000		
Sensory organs	0.0118		
White blood cells	0.0009		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0154
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0082
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0297
Endocrine tissue	0.0245
Fetal	0.0082
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0032
Testicles	0.0156
Lungs	0.0000
Nerves	0.0080
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 36

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0046	0.0077	0.6062 1.6497
Bladder	0.0013	0.0153	0.0874 11.4458
Breast	0.0091	0.0026	3.5059 0.2852
Ovary	0.0036	0.0054	0.6698 1.4930
Endocrine tissue	0.0174	0.0048	3.6642 0.2729
Gastrointestinal	0.0034	0.0000	undef 0.0000
Brain	0.0028	0.0000	undef 0.0000
Hematopoietic	0.0249	0.0000	undef 0.0000
Skin	0.0248	0.0000	undef 0.0000
Hepatic	0.0032	0.0137	0.2312 4.3248
Heart	0.0000	0.0000	undef undef
Testicles	0.0261	0.0095	2.7652 0.3616
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0297	0.0000	undef 0.0000
Pancreas	0.0095	0.0000	undef 0.0000
Penis	0.0000	0.0000	undef undef
Prostate	0.0143	0.0064	2.2373 0.4470
Uterus	0.0050	0.0000	undef 0.0000
Breast hyperplasia	0.0145		
Small intestine	0.0031		
Prostatic hyperplasia	0.0149		
Seminal vesicles	0.0089		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

	0.0000
Development	0.0031
Gastrointestinal	0.0000
Brain	0.0039
Hematopoietic	0.0041
Heart-blood vessels	0.0074
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	0.0000
Breast	0.0046
Ovary-uterus	0.0000
Endocrine tissue	0.0029
Fetal	0.0244
Gastrointestinal	0.0000
Hematopoietic	0.0032
Skin-muscle	0.0000
Testicles	0.0246
Lungs	0.0010
Nerves	0.0064
Prostate	0.0000
Sensory organs	

Electronic Northern Blot for SEQ. ID. NO: 37

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0093	0.0000	undef	0.0000
Bladder	0.0013	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Ovary	0.0018	0.0000	undef	0.0000
Endocrine tissue	0.0039	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0012	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0095	0.0021	4.4745	0.2235
Uterus	0.0050	0.0356	0.1393	7.1813
Breast hyperplasia	0.0000			
Small intestine	0.0093			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

	0.0000
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	0.0000
Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 39

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0325	0.0332	0.9792 1.0213
Bladder	0.0293	0.0196	1.4950 0.6689
Breast	0.0000	0.0104	0.0000 undef
Ovary	0.0091	0.0000	undef 0.0000
Endocrine tissue	0.0252	0.0000	undef 0.0000
Gastrointestinal	0.0085	0.0131	0.6451 1.5502
Brain	0.0098	0.0000	undef 0.0000
Hematopoietic	0.0249	0.0000	undef 0.0000
Skin	0.0000	0.0065	0.0000 undef
Hepatic	0.0636	0.1649	0.3854 2.5949
Heart	0.0183	0.0000	undef 0.0000
Testicles	0.0212	0.0165	1.2792 0.7818
Lungs	0.0000	0.0153	0.0000 undef
Stomach-esophagus	0.0137	0.0060	2.2841 0.4378
Muscle-skeleton	0.0208	0.0137	1.5196 0.6581
Kidneys	0.0284	0.0166	1.7142 0.5834
Pancreas	0.0000	0.0533	0.0000 undef
Penis	0.0048	0.0106	0.4475 2.2349
Prostate	0.0033	0.0000	undef 0.0000
Uterus	0.0036		
Breast hyperplasia	0.0218		
Small intestine	0.0119		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0588		
Sensory organs	0.1045		
White blood cells			

FETUS
% freq.

	0.0154
Development	0.0123
Gastrointestinal	0.0000
Brain	0.0118
Hematopoietic	0.0041
Heart-blood vessels	0.0148
Lungs	0.0000
Kidneys	0.0249
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	0.0000
Breast	0.0114
Ovary-uterus	0.1224
Endocrine tissue	0.0122
Fetal	0.0366
Gastrointestinal	0.0000
Hematopoietic	0.0291
Skin-muscle	0.0000
Testicles	0.0164
Lungs	0.0040
Nerves	0.0385
Prostate	0.0000
Sensory organs	

Electronic Northern Blot for SEQ. ID. NO: 41

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0022	0.0000	undef
Ovary	0.0061	0.0026	2.3372	0.4279
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0050	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0048	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0059			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0078
Lungs	0.0082
Nerves	0.0010
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 42

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0160	0.0044	3.6695	0.2725
Ovary	0.0030	0.0026	1.1686	0.8557
Endocrine tissue	0.0109	0.0082	1.3396	0.7465
Gastrointestinal	0.0078	0.0000	undef	0.0000
Brain	0.0042	0.0055	0.7741	1.2918
Hematopoietic	0.0070	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0037	0.0024	1.5801	0.6329
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidneys	0.0059	0.0000	undef	0.0000
Pancreas	0.0057	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0167	0.0000	undef	0.0000
Uterus	0.0066	0.0000	undef	0.0000
Breast hyperplasia	0.0109			
Small intestine	0.0031			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0070
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0256
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 44

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0372	0.0230	1.6164 0.6186
Bladder	0.0067	0.0000	undef 0.0000
Breast	0.0122	0.0130	0.9349 1.0696
Ovary	0.0128	0.0300	0.4262 2.3462
Endocrine tissue	0.0271	0.0333	0.8143 1.2281
Gastrointestinal	0.0059	0.0471	0.1260 7.9354
Brain	0.0056	0.0000	undef 0.0000
Hematopoietic	0.0099	0.0000	undef 0.0000
Skin	0.0050	0.0259	0.1913 5.2277
Hepatic	0.0201	0.0137	1.4644 0.6829
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0274	0.0189	1.4485 0.6904
Lungs	0.0290	0.0000	undef 0.0000
Stomach-esophagus	0.0103	0.0000	undef 0.0000
Muscle-skeleton	0.0089	0.0137	0.6512 1.5355
Kidneys	0.0076	0.0166	0.4571 2.1876
Pancreas	0.0150	0.0000	undef 0.0000
Penis	0.0333	0.0106	3.1322 0.3193
Prostate	0.0215	0.0000	undef 0.0000
Uterus	0.0036		
Breast hyperplasia	0.0280		
Small intestine	0.0357		
Prostatic hyperplasia	0.0890		
Seminal vesicles	0.0235		
Sensory organs	0.0052		
White blood cells			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lungs	0.0222
Kidneys	0.0309
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0183
Endocrine tissue	0.0000
Fetal	0.0227
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0162
Testicles	0.0000
Lungs	0.0082
Nerves	0.0050
Prostate	0.0256
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 46

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0040	0.0131	0.3058 3.2702
Breast	0.0122	0.0234	0.5194 1.9254
Ovary	0.0036	0.0109	0.3349 2.9861
Endocrine tissue	0.0116	0.0095	1.2214 0.8187
Gastrointestinal	0.0051	0.0164	0.3096 3.2295
Brain	0.0028	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0085	0.0137	0.6166 1.6218
Heart	0.0061	0.0117	0.5224 1.9144
Testicles	0.0075	0.0095	0.7901 1.2657
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0051	0.0000	undef 0.0000
Muscle-skeleton	0.0030	0.0068	0.4342 2.3033
Kidneys	0.0076	0.0055	1.3713 0.7292
Pancreas	0.0030	0.0000	undef 0.0000
Penis	0.0119	0.0043	2.7966 0.3576
Prostate	0.0083	0.0071	1.1604 0.8618
Uterus	0.0036		
Breast hyperplasia	0.0093		
Small intestine	0.0030		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0118		
Sensory organs	0.0026		
White blood cells			

FETUS
% freq.

	0.0000
Development	0.0154
Gastrointestinal	0.0125
Brain	0.0157
Hematopoietic	0.0041
Heart-blood vessels	0.0037
Lungs	0.0062
Kidneys	0.0000
Prostate	0.0140
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0245
Fetal	0.0117
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0000
Lungs	0.0164
Nerves	0.0110
Prostate	0.0192
Sensory organs	0.0000

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0077	1.2123	0.8249
Breast	0.0093	0.0283	0.3293	3.0366
Ovary	0.0182	0.0052	3.5059	0.2852
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0504	0.0000	undef	0.0000
Brain	0.0000	0.0033	0.0000	undef
Hematopoietic	0.0042	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0495	0.0065	7.6515	0.1307
Heart	0.0074	0.0137	0.5395	1.8535
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0120	0.0060	1.9985	0.5004
Kidneys	0.0238	0.0000	undef	0.0000
Pancreas	0.0511	0.0276	1.8513	0.5402
Penis	0.0000	0.0000	undef	undef
Prostate	0.0333	0.0149	2.2373	0.4470
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0109			
Small intestine	0.1028			
Prostatic hyperplasia	0.0059			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0183			

Development	0.0000
Gastrointestinal	0.0462
Brain	0.0000
Hematopoietic	0.0197
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0249
Sensory organs	0.0000

Breast	0.0000
Ovary-uterus	0.0160
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0324
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0256
	0.0000

Electronic Northern Blot for SEQ. ID. NO: 51

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0465	0.0741	0.6271 1.5947
Breast	0.0386	0.0501	0.7711 1.2968
Breast	0.0334	0.0546	0.6121 1.6336
Ovary	0.0310	0.0300	1.0351 0.9661
Endocrine tissue	0.0252	0.0190	1.3232 0.7558
Gastrointestinal	0.0458	0.0701	0.6532 1.5310
Brain	0.0112	0.1135	0.0986 10.1456
Hematopoietic	0.0448	0.0000	undef 0.0000
Skin	0.0347	0.0000	undef 0.0000
Hepatic	0.1123	0.1375	0.8170 1.2240
Heart	0.0366	0.0468	0.7835 1.2763
Testicles	0.0535	0.0449	1.1920 0.8389
Lungs	0.0193	0.0153	1.2599 0.7937
Stomach-esophagus	0.0685	0.1860	0.3684 2.7145
Muscle-skeleton	0.0119	0.0890	0.1336 7.4857
Kidneys	0.0151	0.0828	0.1828 5.4691
Pancreas	0.1018	0.0533	1.9092 0.5238
Penis	0.0167	0.0064	2.6101 0.3831
Prostate	0.0545	0.2634	0.2070 4.8311
Uterus	0.0981		
Breast hyperplasia	0.0312		
Small intestine	0.0386		
Prostatic hyperplasia	0.0178		
Seminal vesicles	0.0235		
Sensory organs	0.0009		
White blood cells			

FETUS
% freq.

Development	0.1383
Gastrointestinal	0.0924
Brain	0.0063
Hematopoietic	0.0393
Heart-blood vessels	0.0654
Lungs	0.0592
Kidneys	0.0309
Prostate	0.2992
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Ovary-uterus	0.0068
Endocrine tissue	0.0000
Fetal	0.0099
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0171
Prostate	0.0000
Sensory organs	0.0387

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0013	0.0022	0.6116	1.6351
Breast	0.0030	0.0000	undef	0.0000
Ovary	0.0036	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0008	0.0099	0.0860	11.6263
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0061	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0059	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0119	0.0021	5.5932	0.1788
Uterus	0.0083	0.0000	undef	0.0000
Breast hyperplasia	0.0036			
Small intestine	0.0000			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0136
Ovary-uterus	0.0114
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0040
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 53

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0051	0.0000 undef
Breast	0.0000	0.0044	0.0000 undef
Ovary	0.0030	0.0000	undef 0.0000
Endocrine tissue	0.0055	0.0027	2.0093 0.4977
Gastrointestinal	0.0058	0.0048	1.2214 0.8187
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0032	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lungs	0.0000	0.0024	0.0000 undef
Stomach-esophagus	0.0000	0.0153	0.0000 undef
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Prostate	0.0071	0.0021	3.3559 0.2980
Uterus	0.0033	0.0000	undef 0.0000
Breast hyperplasia	0.0036		
Small intestine	0.0000		
Prostatic hyperplasia	0.0030		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 54

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0077	1.2123 0.8249
Breast	0.0200	0.0044	4.5868 0.2180
Ovary	0.0152	0.0104	1.4608 0.6846
Endocrine tissue	0.0091	0.0054	1.6745 0.5972
Gastrointestinal	0.0039	0.0048	0.8143 1.2281
Brain	0.0110	0.0033	3.3545 0.2981
Hematopoietic	0.0056	0.0000	undef 0.0000
Skin	0.0149	0.0000	undef 0.0000
Hepatic	0.0198	0.0000	undef 0.0000
Heart	0.0064	0.0000	undef 0.0000
Testicles	0.0122	0.0000	undef 0.0000
Lungs	0.0062	0.0071	0.8779 1.1391
Stomach-esophagus	0.0097	0.0000	undef 0.0000
Muscle-skeleton	0.0051	0.0240	0.2141 4.6701
Kidneys	0.0178	0.0000	undef 0.0000
Pancreas	0.0019	0.0110	0.1714 5.8337
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0119	0.0043	2.7966 0.3576
Uterus	0.0050	0.0214	0.2321 4.3088
Breast hyperplasia	0.0000		
Small intestine	0.0062		
Prostatic hyperplasia	0.0208		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0540		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0250
Hematopoietic	0.0275
Heart-blood vessels	0.0082
Lungs	0.0037
Kidneys	0.0185
Prostate	0.0000
Sensory organs	0.0558

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0000
Lungs	0.0082
Nerves	0.0040
Prostate	0.0064
Sensory organs	0.0310

Electronic Northern Blot for SEQ. ID. NO: 55

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0153	0.6062 1.6497
Breast	0.0053	0.0065	0.8154 1.2263
Ovary	0.0000	0.0052	0.0000 undef
Endocrine tissue	0.0055	0.0054	1.0047 0.9954
Gastrointestinal	0.0039	0.0048	0.8143 1.2281
Brain	0.0042	0.0033	1.2902 0.7751
Hematopoietic	0.0028	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0050	0.0129	0.3826 2.6139
Heart	0.0074	0.0000	undef 0.0000
Testicles	0.0061	0.0234	0.2612 3.8288
Lungs	0.0100	0.0095	1.0534 0.9493
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidneys	0.0089	0.0137	0.6512 1.5355
Pancreas	0.0057	0.0000	undef 0.0000
Penis	0.0030	0.0000	undef 0.0000
Prostate	0.0048	0.0021	2.2373 0.4470
Uterus	0.0066	0.0071	0.9283 1.0772
Breast hyperplasia	0.0036		
Small intestine	0.0000		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0089		
Sensory organs	0.0118		
White blood cells	0.0026		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0082
Nerves	0.0010
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 58

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0026	3.6370	0.2750
Breast	0.0080	0.0022	3.6695	0.2725
Breast	0.0061	0.0078	0.7791	1.2836
Ovary	0.0018	0.0109	0.1674	5.9721
Endocrine tissue	0.0078	0.0143	0.5428	1.8422
Gastrointestinal	0.0034	0.0033	1.0321	0.9689
Brain	0.0084	0.0000	undef	0.0000
Hematopoietic	0.0895	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0032	0.0137	0.2312	4.3248
Heart	0.0183	0.0000	undef	0.0000
Testicles	0.0037	0.0142	0.2634	3.7971
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0068	0.0000	undef
Kidneys	0.0038	0.0000	undef	0.0000
Pancreas	0.0090	0.0000	undef	0.0000
Penis	0.0071	0.0021	3.3559	0.2980
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0182			
Breast hyperplasia	0.0031			
Small intestine	0.0030			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Brain	0.0157
Hematopoietic	0.0082
Heart-blood vessels	0.0148
Lungs	0.0124
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0160
Endocrine tissue	0.0245
Fetal	0.0082
Gastrointestinal	0.0122
Hematopoietic	0.0057
Skin-muscle	0.0032
Testicles	0.0156
Lungs	0.0082
Nerves	0.0080
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 60

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0046	0.0000	undef	0.0000
Breast	0.0040	0.0022	1.8347	0.5450
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0054	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0068	0.0033	2.0643	0.4844
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0050	0.0000	undef	0.0000
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0061	0.0000	undef	0.0000
Lungs	0.0050	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0071	0.0000	undef	0.0000
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0073			
Small intestine	0.0000			
Prostatic hyperplasia	0.0059			
Seminal vesicles	0.0000			
Sensory organs	0.0235			
White blood cells	0.0026			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0000
Nerves	0.0010
Prostate	0.0000
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 61

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0128	0.0000 undef
Breast	0.0000	0.0022	0.0000 undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0018	0.0109	0.1674 5.9721
Gastrointestinal	0.0078	0.0000	undef 0.0000
Brain	0.0034	0.0033	1.0321 0.9689
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0050	0.0000	undef 0.0000
Heart	0.0032	0.0000	undef 0.0000
Testicles	0.0183	0.0000	undef 0.0000
Lungs	0.0025	0.0071	0.3511 2.8478
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0051	0.0000	undef 0.0000
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0019	0.0110	0.1714 5.8337
Penis	0.0120	0.0000	undef 0.0000
Prostate	0.0071	0.0021	3.3559 0.2980
Uterus	0.0033	0.0000	undef 0.0000
Breast hyperplasia	0.0000		
Small intestine	0.0093		
Prostatic hyperplasia	0.0030		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0009		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0188
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0164
Nerves	0.0050
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 62

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0046	0.0026	1.8185 0.5499
Breast	0.0133	0.0022	6.1158 0.1635
Ovary	0.0061	0.0052	1.1686 0.8557
Endocrine tissue	0.0000	0.0245	0.0000 undef
Gastrointestinal	0.0078	0.0190	0.4071 2.4562
Brain	0.0119	0.0022	5.4187 0.1845
Hematopoietic	0.0070	0.0757	0.0924 10.8219
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0099	0.0000	undef 0.0000
Heart	0.0074	0.0275	0.2698 3.7070
Testicles	0.0000	0.0234	0.0000 undef
Lungs	0.0050	0.0118	0.4214 2.3732
Stomach-esophagus	0.0097	0.0153	0.6300 1.5874
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidneys	0.0119	0.0205	0.5789 1.7275
Pancreas	0.0038	0.0000	undef 0.0000
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0191	0.0043	4.4745 0.2235
Uterus	0.0066	0.0000	undef 0.0000
Breast hyperplasia	0.0000		
Small intestine	0.0031		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0070		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0082
Heart-blood vessels	0.0037
Lungs	0.0309
Kidneys	0.0000
Prostate	0.0140
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0183
Endocrine tissue	0.0000
Fetal	0.0140
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles	0.0000
Lungs	0.0000
Nerves	0.0161
Prostate	0.0128
Sensory organs	0.0155

Electronic Northern Blot for SEQ. ID. NO: 63

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0186	0.0844	0.2204 4.5368
Breast	0.0560	0.0370	1.5110 0.6618
Ovary	0.0395	0.0260	1.5192 0.6582
Endocrine tissue	0.0128	0.0245	0.5209 1.9196
Gastrointestinal	0.0775	0.0857	0.9047 1.1053
Brain	0.0254	0.0350	0.7257 1.3779
Hematopoietic	0.0364	0.0378	0.9610 1.0406
Skin	0.2188	0.0000	undef 0.0000
Hepatic	0.0198	0.0582	0.3401 2.9406
Heart	0.1112	0.1787	0.6225 1.6064
Testicles	0.0183	0.0117	1.5671 0.6381
Lungs	0.1133	0.0804	1.4097 0.7094
Stomach-esophagus	0.0676	0.0307	2.2049 0.4535
Muscle-skeleton	0.1696	0.0300	5.6530 0.1769
Kidneys	0.0684	0.0753	0.9078 1.1016
Pancreas	0.0151	0.0607	0.2493 4.0107
Penis	0.0749	0.1066	0.7019 1.4246
Prostate	0.0715	0.0106	6.7118 0.1490
Uterus	0.0611	0.0214	2.8624 0.3494
Breast hyperplasia	0.0254		
Small intestine	0.0997		
Prostatic hyperplasia	0.0386		
Seminal vesicles	0.0445		
Sensory organs	0.0941		
White blood cells	0.0670		

FETUS
% freq.

Development	0.0615
Gastrointestinal	0.0154
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0041
Lungs	0.0074
Kidneys	0.0185
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0408
Ovary-uterus	0.0114
Endocrine tissue	0.0000
Fetal	0.0338
Gastrointestinal	0.1098
Hematopoietic	0.0114
Skin-muscle	0.0421
Testicles	0.0312
Lungs	0.2786
Nerves	0.0080
Prostate	0.0192
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 64

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0093	0.0153	0.6062 1.6497
Breast	0.0160	0.0174	0.9174 1.0901
Ovary	0.0091	0.0182	0.5008 1.9967
Endocrine tissue	0.0201	0.0109	1.8419 0.5429
Gastrointestinal	0.0194	0.0333	0.5816 1.7193
Brain	0.0076	0.0219	0.3483 2.8707
Hematopoietic	0.0182	0.0378	0.4805 2.0811
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0099	0.0323	0.3061 3.2673
Heart	0.0148	0.0275	0.5395 1.8535
Testicles	0.0122	0.0000	undef 0.0000
Lungs	0.0174	0.0118	1.4748 0.6781
Stomach-esophagus	0.0290	0.0307	0.9449 1.0583
Muscle-skeleton	0.0154	0.0120	1.2848 0.7783
Kidneys	0.0416	0.0068	6.0782 0.1645
Pancreas	0.0170	0.0110	1.5428 0.6482
Penis	0.0120	0.0267	0.4492 2.2260
Prostate	0.0191	0.0085	2.2373 0.4470
Uterus	0.0149	0.0142	1.0444 0.9575
Breast hyperplasia	0.0182		
Small intestine	0.0187		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0178		
Sensory organs	0.0353		
White blood cells	0.0183		

FETUS
% freq.

Development	0.0307
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0393
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0124
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0476
Ovary-uterus	0.0571
Endocrine tissue	0.0245
Fetal	0.0175
Gastrointestinal	0.0244
Hematopoietic	0.0114
Skin-muscle	0.0291
Testicles	0.0000
Lungs	0.0082
Nerves	0.0020
Prostate	0.0000
Sensory organs	0.0310

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0100	0.0136	0.7358	1.3590
Bladder	0.0039	0.0094	0.4149	2.4102
Breast	0.0053	0.0028	1.8786	0.5323
Large intestine	0.0153	0.0028	5.3823	0.1858
Small intestine	0.0027	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0032	0.0114	0.2826	3.5381
Brain	0.0072	0.0060	1.2090	0.8271
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0046	0.0127	0.3662	2.7307
Heart	0.0071	0.0137	0.5169	1.9348
Testicles	0.0080	0.0059	1.3570	0.7369
Lung	0.0107	0.0037	2.8941	0.3455
Stomach-esophagus	0.0000	0.0064	0.0000	undef
Muscle-skeleton	0.0086	0.0000	undef	0.0000
Kidney	0.0045	0.0048	0.9284	1.0771
Pancreas	0.0116	0.0055	2.0940	0.4776
Prostate	0.0038	0.0013	2.8940	0.3455
T lymphoma	0.0025	0.0075	0.3381	2.9576
Uterus	0.0031	0.0092	0.3368	2.9694
White blood cells	0.0089	0.0000	undef	0.0000
Hematopoietic	0.0067			
Penis	0.0054			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

- Development
- Gastrointestinal
- Brain
- Hematopoietic
- Skin
- Hepatic
- Heart-blood vessels
- Lung
- Adrenal gland
- Kidney
- Placenta
- Prostate
- Sensory organs

Breast	0.0204
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0046
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles_n	0.0167
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0070
Kidney t	0.0000
Ovary Uterus	0.0203
Prostate n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 218

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0075	0.0000	undef	0.0000
Bladder	0.0078	0.0117	0.6638	1.5064
Breast	0.0114	0.0169	0.6784	1.4741
Large intestine	0.0115	0.0085	1.3456	0.7432
Small intestine	0.0110	0.0107	1.0306	0.9703
Ovary	0.0059	0.0072	0.8295	1.2055
Endocrine tissue	0.0144	0.0038	3.8156	0.2621
Brain	0.0193	0.0110	1.7586	0.5686
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0000	0.0190	0.0000	undef
Heart	0.0173	0.0137	1.2552	0.7967
Testicles	0.0080	0.0059	1.3570	0.7369
Lung	0.0165	0.0111	1.4909	0.6707
Stomach-esophagus	0.0000	0.0128	0.0000	undef
Muscle-skeleton	0.0051	0.0037	1.3917	0.7186
Kidney	0.0179	0.0048	3.7136	0.2693
Pancreas	0.0033	0.0442	0.0748	13.3714
Prostate	0.0085	0.0039	2.1705	0.4607
T lymphoma	0.0101	0.0075	1.3525	0.7394
Uterus	0.0093	0.0138	0.6735	1.4847
White blood cells	0.0096	0.0304	0.3156	3.1685
Hematopoietic	0.0094			
Penis	0.0134			
Seminal vesicle	0.0352			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0188
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0185
Placenta	0.0182
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0244
Hematopoietic	0.0513
Skin-muscle	0.0194
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0586
Nerves	0.0000
Kidney t	0.0161
Ovary uterus	0.0000
Prostate n	0.0068
Sensory organs	0.0182
White blood cells	0.0077
	0.0000

Electronic Northern for Seq. ID: 219

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0075	0.0000	undef 0.0000
Bladder	0.0156	0.0047	3.3190 0.3013
Breast	0.0185	0.0211	0.8767 1.1406
Large intestine	0.0307	0.0199	1.5378 0.6503
Small intestine	0.0082	0.0213	0.3865 2.5875
Ovary	0.0059	0.0334	0.1778 5.6255
Endocrine tissue	0.0305	0.0266	1.1468 0.8720
Brain	0.0393	0.0189	2.0767 0.4815
Skin	0.0257	0.0000	undef 0.0000
Hepatic	0.0000	0.0127	0.0000 undef
Heart	0.0447	0.0000	undef 0.0000
Testicles	0.0161	0.0118	1.3571 0.7369
Lung	0.0282	0.0240	1.1739 0.8519
Stomach-esophagus	0.0072	0.0000	undef 0.0000
Muscle-skeleton	0.0154	0.0074	2.0875 0.4790
Kidney	0.0269	0.0193	1.3927 0.7180
Pancreas	0.0066	0.0000	undef 0.0000
Prostate	0.0179	0.0065	2.7494 0.3637
T lymphoma	0.0177	0.0672	0.2630 3.8026
Uterus	0.0118	0.0046	2.5703 0.3891
White blood cells	0.0226	0.0000	undef 0.0000
Hematopoietic	0.0147		
Penis	0.0188		
Seminal vesicle	0.0281		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0167
Brain	0.0188
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0356
Lung	0.0145
Adrenal gland	0.0254
Kidney	0.0185
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0292
Testicles_n	0.0167
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0311
Kidney t	0.0000
Ovary uterus	0.0090
Prostate n	0.0061
Sensory organs	0.0310
White blood cells	0.0000

Electronic Northern for Seq. ID: 220

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0050	0.0000	undef	0.0000
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0088	0.0070	1.2524	0.7985
Large intestine	0.0153	0.0085	1.7941	0.5574
Small intestine	0.0192	0.0213	0.9018	1.1089
Ovary	0.0059	0.0262	0.2262	4.4200
Endocrine tissue	0.0337	0.0142	2.3766	0.4208
Brain	0.0156	0.0070	2.2381	0.4468
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0093	0.0063	1.4649	0.6826
Heart	0.0183	0.0000	undef	0.0000
Testicles	0.0161	0.0059	2.7142	0.3684
Lung	0.0185	0.0111	1.6663	0.6001
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0037	1.3917	0.7186
Kidney	0.0157	0.0048	3.2497	0.3077
Pancreas	0.0099	0.0055	1.7949	0.5571
Prostate	0.0160	0.0065	2.4600	0.4065
T lymphoma	0.0152	0.0299	0.5072	1.9717
Uterus	0.0089	0.0046	1.9277	0.5188
White blood cells	0.0164	0.0304	0.5410	1.8483
Hematopoietic	0.0040			
Penis	0.0080			
Seminal vesicle	0.0141			
Sensory organs	0.0118			

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0056
Brain	0.0063
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0178
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0058
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0090
Kidney t	0.0000
Ovary uterus	0.0090
Prostate n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 221

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0100	0.0000	undef	0.0000
Bladder	0.0078	0.0047	1.6595	0.6026
Breast	0.0079	0.0056	1.4090	0.7097
Large intestine	0.0057	0.0085	0.6728	1.4864
Small intestine	0.0082	0.0000	undef	0.0000
Ovary	0.0030	0.0143	0.2074	4.8219
Endocrine tissue	0.0112	0.0106	1.0563	0.9467
Brain	0.0052	0.0040	1.3056	0.7659
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0063	0.0000	undef
Heart	0.0132	0.0000	undef	0.0000
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0117	0.0129	0.9021	1.1085
Stomach-esophagus	0.0000	0.0064	0.0000	undef
Muscle-skeleton	0.0086	0.0074	1.1597	0.8623
Kidney	0.0179	0.0048	3.7139	0.2693
Pancreas	0.0083	0.0000	undef	0.0000
Prostate	0.0113	0.0065	1.7364	0.5759
T lymphoma	0.0000	0.0149	0.0000	undef
Uterus	0.0044	0.0046	0.9638	1.0375
White blood cells	0.0075	0.0304	0.2480	4.0326
Hematopoietic	0.0067			
Penis	0.0080			
Seminal vesicle	0.0141			
Sensory organs	0.0118			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0242
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0050
Kidney t	0.0000
Ovary Uterus	0.0000
Prostate n	0.0121
Sensory organs	0.0774
White blood cells	0.0000

Electronic Northern for Seq. ID: 222

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0351	0.0047	7.4677	0.1339
Breast	0.0070	0.0014	5.0097	0.1996
Large intestine	0.0115	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0024	0.0000	undef
Endocrine tissue	0.0016	0.0035	0.4527	2.2091
Brain	0.0017	0.0060	0.2901	3.4467
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0063	0.0000	undef
Heart	0.0020	0.0137	0.1477	6.7715
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0039	0.0018	2.1049	0.4751
Stomach-esophagus	0.0145	0.0000	undef	0.0000
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0112	0.0000	undef	0.0000
Pancreas	0.0017	0.0055	0.2992	3.3427
Prostate	0.0075	0.0026	2.8941	0.3455
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0059	0.0046	1.2851	0.7781
White blood cells	0.0027	0.0000	undef	0.0000
Hematopoietic	0.0013			
Penis	0.0054			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0254
Kidney	0.0185
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0340
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0020
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 223

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0100	0.0000	undef	0.0000
Bladder	0.0273	0.0117	2.3233	0.4304
Breast	0.0150	0.0098	1.5208	0.6576
Large intestine	0.0077	0.0028	2.6911	0.3716
Small intestine	0.0110	0.0000	undef	0.0000
Ovary	0.0089	0.0024	3.7330	0.2679
Endocrine tissue	0.0016	0.0053	0.3018	3.3136
Brain	0.0069	0.0100	0.6963	1.4361
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0190	0.0000	undef
Heart	0.0081	0.0137	0.5907	1.6929
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0068	0.0111	0.6139	1.6289
Stomach-esophagus	0.0072	0.0128	0.5668	1.7644
Muscle-skeleton	0.0086	0.0037	2.3194	0.4311
Kidney	0.0112	0.0000	undef	0.0000
Pancreas	0.0050	0.0055	0.8975	1.1142
Prostate	0.0141	0.0169	0.8348	1.1978
T lymphoma	0.0202	0.0075	2.7049	0.3697
Uterus	0.0177	0.0000	undef	0.0000
White blood cells	0.0096	0.0000	undef	0.0000
Hematopoietic	0.0187			
Penis	0.0080			
Seminal vesicle	0.0281			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0046
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0010
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0121
Sensory organs	0.0155
White blood cells	0.0000

Electronic Northern for Seq. ID: 224

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0050	0.0000	undef	0.0000
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0018	0.0112	0.1566	6.3876
Large intestine	0.0057	0.0057	1.0092	0.9909
Small intestine	0.0027	0.0000	undef	0.0000
Ovary	0.0059	0.0143	0.4148	2.4109
Endocrine tissue	0.0032	0.0053	0.6036	1.6568
Brain	0.0029	0.0060	0.4835	2.0680
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0093	0.0000	undef	0.0000
Heart	0.0051	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0039	0.0037	1.0524	0.9502
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0037	0.4639	2.1557
Kidney	0.0112	0.0048	2.3212	0.4308
Pancreas	0.0099	0.0055	1.7949	0.5571
Prostate	0.0066	0.0065	1.0129	0.9872
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0034	0.0000	undef	0.0000
Hematopoietic	0.0053			
Penis	0.0080			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0107
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0030
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0000
Sensory organs	0.0243
White blood cells	0.0000

Electronic Northern for Seq. ID: 225

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0075	0.0136	0.5519 1.8120
Bladder	0.0078	0.0023	3.3190 0.3013
Breast	0.0053	0.0056	0.9393 1.0646
Large intestine	0.0057	0.0000	undef 0.0000
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0059	0.0072	0.8296 1.2055
Endocrine tissue	0.0177	0.0018	9.9589 0.1004
Brain	0.0075	0.0050	1.5087 0.6628
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0127	0.0000 undef
Heart	0.0061	0.0000	undef 0.0000
Testicles	0.0161	0.0000	undef 0.0000
Lung	0.0088	0.0111	0.7893 1.2669
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0034	0.0074	0.4639 2.1557
Kidney	0.0090	0.0048	1.8570 0.5385
Pancreas	0.0099	0.0055	1.7949 0.5571
Prostate	0.0113	0.0013	8.6822 0.1152
T lymphoma	0.0025	0.0075	0.3381 2.9576
Uterus	0.0059	0.0046	1.2851 0.7781
White blood cells	0.0034	0.0000	undef 0.0000
Hematopoietic	0.0053		
Penis	0.0080		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0182
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0127
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0167
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0040
Ovary uterus	0.0000
Prostate n	0.0180
Sensory organs	0.0061
White blood cells	0.0000

Electronic Northern for Seq. ID: 226

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0023	0.0000	undef
Breast	0.0053	0.0056	0.9393	1.0646
Large intestine	0.0057	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Brain	0.0016	0.0053	0.3018	3.3136
Skin	0.0035	0.0020	1.7408	0.5745
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0046	0.0000	undef	0.0000
Testicles	0.0010	0.0000	undef	0.0000
Lung	0.0000	0.0059	0.0000	undef
Stomach-esophagus	0.0019	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0045	0.0048	0.9285	1.0770
Prostate	0.0033	0.0000	undef	0.0000
T lymphoma	0.0038	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0059	0.0046	1.2851	0.7781
Hematopoietic	0.0027	0.0000	undef	0.0000
Penis	0.0000			
Seminal vesicle	0.0080			
Sensory organs	0.0000			
	0.0118			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0046
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0070
Ovary Uterus	0.0000
Prostate n	0.0023
Sensory Organs	0.0182
White blood cells	0.0077
	0.0000

Electronic Northern for Seq. ID: 227

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0038	0.0000	undef 0.0000
Bladder	0.0000	0.0094	0.0000 undef
Breast	0.0025	0.0089	0.2799 3.5727
Large intestine	0.0057	0.0228	0.2523 3.9638
Small intestine	0.0082	0.0000	undef 0.0000
Ovary	0.0059	0.0095	0.6222 1.6073
Endocrine tissue	0.0096	0.0033	2.9275 0.3416
Brain	0.0134	0.0050	2.6904 0.3717
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0093	0.0063	1.4649 0.6826
Heart	0.0081	0.0137	0.5907 1.6928
Testicles	0.0161	0.0000	undef 0.0000
Lung	0.0049	0.0037	1.3158 0.7600
Stomach-esophagus	0.0000	0.0165	0.0000 undef
Muscle-skeleton	0.0000	0.0074	0.0000 undef
Kidney	0.0112	0.0000	undef 0.0000
Pancreas	0.0033	0.0092	0.3604 2.7748
Prostate	0.0113	0.0078	1.4470 0.6911
T lymphoma	0.0033	0.0173	0.1901 5.2613
Uterus	0.0118	0.0046	2.5702 0.3891
White blood cells	0.0023	0.0000	undef 0.0000
Hematopoietic	0.0047		
Penis	0.0027		
Seminal vesicle	0.0000		
Sensory organs	0.0118		

FETUS % freq.

Development	0.0278
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0036
Heart-blood vessels	0.0108
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0125
Ovary t	0.0379
Endocrine tissue	0.0000
Fetal	0.0066
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0090
Testicles_n	0.0169
Testicles_t	0.0228
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0191
Ovary uterus	0.0495
Prostate n	0.0325
Sensory organs	0.0182
	0.0077

Electronic Northern for Seq. ID: 228

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0000	0.0094	0.0000	undef
Breast	0.0070	0.0056	1.2524	0.7985
Large intestine	0.0057	0.0000	undef	0.0000
Small intestine	0.0055	0.0000	undef	0.0000
Ovary	0.0146	0.0048	3.1108	0.3215
Endocrine tissue	0.0016	0.0018	0.9054	1.1045
Brain	0.0064	0.0060	1.0638	0.9400
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0127	0.0000	undef
Heart	0.0030	0.0000	undef	0.0000
Testicles	0.0080	0.0118	0.6786	1.4737
Lung	0.0019	0.0074	0.2631	3.9007
Stomach-esophagus	0.0145	0.0000	undef	0.0000
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0045	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Prostate	0.0057	0.0026	2.1706	0.4607
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0015	0.0046	0.3213	3.1125
White blood cells	0.0048	0.0000	undef	0.0000
Hematopoietic	0.0067			
Penis	0.0027			
Seminal vesicle	0.0070			
Sensory organs	0.0118			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0121
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0245
Fetal	0.0017
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0060
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0182
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 229

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0039	0.0023	1.6595	0.6026
Breast	0.0018	0.0000	undef	0.0000
Large intestine	0.0019	0.0028	0.6728	1.4864
Small intestine	0.0027	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0016	0.0000	undef	0.0000
Brain	0.0000	0.0020	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0059	0.0000	undef
Stomach-esophagus	0.0010	0.0018	0.5262	1.9004
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0037	0.4639	2.1557
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0017	0.0000	undef	0.0000
T lymphoma	0.0038	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0007	0.0000	undef	0.0000
Penis	0.0000			
Seminal vesicle	0.0027			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0000
Sensory organs	0.0121
White blood cells	0.0000
	0.0000

Electronic Northern for Seq. ID: 230

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0136	0.3679 2.7181
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0053	0.0042	1.2524 0.7985
Large intestine	0.0038	0.0057	0.6728 1.4864
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0148	0.0072	2.0739 0.4822
Endocrine tissue	0.0080	0.0106	0.7545 1.3254
Brain	0.0046	0.0060	0.7737 1.2925
Skin	0.0000	0.0000	undef undef
Hepatic	0.0093	0.0000	undef 0.0000
Heart	0.0041	0.0000	undef 0.0000
Testicles	0.0120	0.0000	undef 0.0000
Lung	0.0010	0.0018	0.5262 1.9004
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0086	0.0185	0.4639 2.1557
Kidney	0.0022	0.0048	0.4642 2.1540
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0019	0.0013	1.4470 0.6911
T lymphoma	0.0000	0.0075	0.0000 undef
Uterus	0.0015	0.0230	0.0643 15.5627
White blood cells	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0027		
Penis	0.0027		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0139
Brain	0.0188
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0151
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles_n	0.0376
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0100
Kidney t	0.0000
Ovary uterus	0.0045
Prostate n	0.0182
Sensory organs	0.0310
White blood cells	0.0000

Electronic Northern for Seq. ID: 231

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0136	0.0000 undef
Bladder	0.0117	0.0047	2.4892 0.4017
Breast	0.0053	0.0028	1.8786 0.5323
Large intestine	0.0038	0.0000	undef 0.0000
Small intestine	0.0110	0.0213	0.5153 1.9406
Ovary	0.0030	0.0072	0.4148 2.4109
Endocrine tissue	0.0064	0.0053	1.2071 0.8284
Brain	0.0064	0.0140	0.4559 2.1934
Skin	0.0110	0.0000	undef 0.0000
Hepatic	0.0000	0.0254	0.0000 undef
Heart	0.0000	0.0137	0.0000 undef
Testicles	0.0000	0.0059	0.0000 undef
Lung	0.0068	0.0055	1.2278 0.8144
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0067	0.0096	0.6964 1.4360
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0104	0.0039	2.6529 0.3769
T lymphoma	0.0025	0.0075	0.3381 2.9576
Uterus	0.0044	0.0000	undef 0.0000
White blood cells	0.0027	0.0000	undef 0.0000
Hematopoietic	0.0013		
Penis	0.0080		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0418
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0098
Nerves	0.0000
Kidney t	0.0030
Ovary Uterus	0.0000
Prostate n	0.0023
Sensory organs	0.0061
White blood cells	0.0000
	0.0000

Electronic Northern for Seq. ID: 232

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0100	0.0136	0.7358 1.3590
Bladder	0.0117	0.0094	1.2446 0.8035
Breast	0.0150	0.0056	2.6614 0.3757
Large intestine	0.0038	0.0199	0.1922 5.2023
Small intestine	0.0110	0.0000	undef 0.0000
Ovary	0.0119	0.0215	0.5530 1.8082
Endocrine tissue	0.0048	0.0053	0.9054 1.1045
Brain	0.0046	0.0040	1.1605 0.8617
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0046	0.0190	0.2441 4.0959
Heart	0.0142	0.0137	1.0337 0.9674
Testicles	0.0080	0.0118	0.6786 1.4737
Lung	0.0078	0.0092	0.8419 1.1877
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0034	0.0074	0.4639 2.1557
Kidney	0.0067	0.0096	0.6964 1.4360
Pancreas	0.0066	0.0000	undef 0.0000
Prostate	0.0123	0.0039	3.1353 0.3190
T lymphoma	0.0101	0.0224	0.4508 2.2182
Uterus	0.0044	0.0046	0.9638 1.0375
White blood cells	0.0062	0.0000	undef 0.0000
Hematopoietic	0.0134		
Penis	0.0134		
Seminal vesicle	0.0000		
Sensory organs	0.0118		

FETUS % freq.

Development	0.0000
Gastrointestinal	0.0139
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0181
Adrenal gland	0.0254
Kidney	0.0000
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0245
Fetal	0.0087
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0376
Testicles_t	0.0000
Lungs_n	0.0293
Lungs_t	0.0000
Nerves	0.0100
Kidney t	0.0000
Ovary uterus	0.0338
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 233

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0000	undef 0.0000
Bladder	0.0078	0.0117	0.6638 1.5065
Breast	0.0088	0.0155	0.5693 1.7566
Large intestine	0.0211	0.0028	7.4006 0.1351
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0119	0.0024	4.9773 0.2009
Endocrine tissue	0.0032	0.0142	0.2263 4.4181
Brain	0.0035	0.0000	undef 0.0000
Skin	0.0257	0.0000	undef 0.0000
Hepatic	0.0279	0.0000	undef 0.0000
Heart	0.0071	0.0137	0.5169 1.9347
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0292	0.0148	1.9733 0.5068
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0269	0.0000	undef 0.0000
Pancreas	0.0165	0.0000	undef 0.0000
Prostate	0.0141	0.0052	2.7132 0.3686
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0044	0.0000	undef 0.0000
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0040	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Seminal vesicle	0.0000		
Sensory organs	0.0070		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0145
Adrenal gland	0.0254
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0058
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0293
Lungs_t	0.0000
Nerves	0.0020
Kidney t	0.0000
Ovary uterus	0.0068
Prostate n	0.0243
Sensory organs	0.0000
White blood cells	0.0000

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0000	0.0094	0.0000	undef
Breast	0.0035	0.0056	0.6262	1.5969
Large intestine	0.0038	0.0000	undef	0.0000
Small intestine	0.0027	0.0000	undef	0.0000
Ovary	0.0059	0.0000	undef	0.0000
Endocrine tissue	0.0048	0.0018	2.7161	0.3682
Brain	0.0035	0.0010	3.4816	0.2872
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0063	0.0000	undef
Heart	0.0020	0.0000	undef	0.0000
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0049	0.0000	undef	0.0000
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0037	0.4639	2.1557
Kidney	0.0022	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Prostate	0.0038	0.0000	undef	0.0000
T lymphoma	0.0126	0.0000	undef	0.0000
Uterus	0.0074	0.0046	1.6064	0.6225
White blood cells	0.0055	0.0304	0.1803	5.5448
Hematopoietic	0.0013			
Penis	0.0000			
Seminal vesicle				
Sensory organs				

	FETUS % freq.
Development	0.0139
Gastrointestinal	0.0139
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
0.0000 % frequency

Breast	0.0000
Breast t	0.0000
Large intestine t	0.0000
Ovary n	0.0000
Ovary t	0.0253
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles n	0.0042
Testicles t	0.0000
Lungs n	0.0000
Lungs t	0.0000
Nerves	0.0090
Kidney t	0.0000
Ovary uterus	0.0113
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 235

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0136	0.0000	undef
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0014	0.0000	undef
Large intestine	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0107	0.0000	undef
Ovary	0.0059	0.0048	1.2443	0.8036
Endocrine tissue	0.0016	0.0053	0.3018	3.3136
Brain	0.0006	0.0030	0.1934	5.1701
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0010	0.0000	undef	0.0000
Testicles	0.0080	0.0000	undef	0.0000
Lung	0.0019	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
T lymphoma	0.0038	0.0000	undef	0.0000
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0046	0.0000	undef
Hematopoietic	0.0007	0.0000	undef	0.0000
Penis	0.0000			
Seminal vesicle	0.0027			
Sensory organs	0.0000			
	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0010
Kidney t	0.0000
Ovary Uterus	0.0023
Prostate n	0.0182
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 236

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0100	0.0000	undef	0.0000
Bladder	0.0000	0.0000	undef	undef
Breast	0.0194	0.0084	2.2961	0.4355
Large intestine	0.0096	0.0000	undef	0.0000
Small intestine	0.0055	0.0000	undef	0.0000
Ovary	0.0059	0.0024	2.4887	0.4018
Endocrine tissue	0.0128	0.0053	2.4143	0.4142
Brain	0.0041	0.0070	0.5803	1.7234
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0051	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0058	0.0092	0.6315	1.5836
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0037	1.3917	0.7186
Kidney	0.0090	0.0000	undef	0.0000
Pancreas	0.0050	0.0000	undef	0.0000
Prostate	0.0104	0.0039	2.6529	0.3769
T lymphoma	0.0025	0.0075	0.3381	2.9576
Uterus	0.0118	0.0000	undef	0.0000
White blood cells	0.0089	0.0000	undef	0.0000
Hematopoietic	0.0134			
Penis	0.0080			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0242
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0093
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0060
Kidney t	0.0000
Ovary Uterus	0.0045
Prostate n	0.0182
Sensory Organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 237

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0176	0.0070	2.5048 0.3992
Large intestine	0.0077	0.0057	1.3456 0.7432
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0030	0.0072	0.4148 2.4109
Endocrine tissue	0.0032	0.0035	0.9054 1.1045
Brain	0.0069	0.0010	6.9631 0.1436
Skin	0.0037	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0061	0.0137	0.4430 2.2572
Testicles	0.0080	0.0000	undef 0.0000
Lung	0.0029	0.0037	0.7893 1.2669
Stomach-esophagus	0.0072	0.0000	undef 0.0000
Muscle-skeleton	0.0000	0.0037	0.0000 undef
Kidney	0.0134	0.0048	2.7855 0.3590
Pancreas	0.0017	0.0055	0.2992 3.3427
Prostate	0.0085	0.0026	3.2558 0.3071
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0074	0.0000	undef 0.0000
White blood cells	0.0027	0.0000	undef 0.0000
Hematopoietic	0.0000		
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0520
Heart-blood vessels	0.0036
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0253
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0070
Ovary Uterus	0.0000
Prostate n	0.0203
Sensory Organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 238

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0075	0.0000	undef 0.0000
Bladder	0.0000	0.0047	0.0000 undef
Breast	0.0009	0.0014	0.6262 1.5969
Large intestine	0.0019	0.0028	0.6728 1.4864
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0148	0.0024	6.2217 0.1607
Endocrine tissue	0.0016	0.0018	0.9054 1.1045
Brain	0.0017	0.0060	0.2901 3.4467
Skin	0.0037	0.0789	0.0466 21.4787
Hepatic	0.0000	0.0000	undef undef
Heart	0.0051	0.0000	undef 0.0000
Testicles	0.0120	0.0118	1.0178 0.9825
Lung	0.0029	0.0018	1.5786 0.6335
Stomach-esophagus	0.0072	0.0000	undef 0.0000
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0000	0.0000	undef 0.0000
Pancreas	0.0017	0.0000	undef undef
Prostate	0.0113	0.0026	4.3411 0.2304
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0030	0.0092	0.3213 3.1125
White blood cells	0.0027	0.0000	undef 0.0000
Hematopoietic	0.0040		
Penis	0.0027		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0060
Ovary uterus	0.0000
Prostate n	0.0068
Sensory organs	0.0061
White blood cells	0.0000

Electronic Northern for Seq. ID: 239

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0125	0.0000	undef 0.0000
Bladder	0.0156	0.0094	1.6595 0.6026
Breast	0.0141	0.0225	0.6262 1.5969
Large intestine	0.0172	0.0085	2.0184 0.4955
Small intestine	0.0192	0.0213	0.9018 1.1089
Ovary	0.0237	0.0262	0.9050 1.1050
Endocrine tissue	0.0144	0.0160	0.9054 1.1045
Brain	0.0197	0.0269	0.7307 1.3686
Skin	0.0184	0.0000	undef 0.0000
Hepatic	0.0279	0.0190	1.4649 0.6826
Heart	0.0203	0.0275	0.7384 1.3543
Testicles	0.0040	0.0059	0.6786 1.4737
Lung	0.0175	0.0166	1.0524 0.9502
Stomach-esophagus	0.0217	0.0000	undef 0.0000
Muscle-skeleton	0.0103	0.0037	2.7833 0.3593
Kidney	0.0112	0.0289	0.3869 2.5849
Pancreas	0.0116	0.0055	2.0941 0.4775
Prostate	0.0141	0.0039	3.6176 0.2764
T lymphoma	0.0025	0.0075	0.3381 2.9576
Uterus	0.0148	0.0184	0.8032 1.2450
White blood cells	0.0068	0.0000	undef 0.0000
Hematopoietic	0.0040		
Penis	0.0134		
Seminal vesicle	0.0070		
Sensory organs	0.0235		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0167
Brain	0.0125
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0213
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0245
Fetal	0.0168
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles_n	0.0125
Testicles_t	0.0000
Lungs_n	0.0098
Lungs-t	0.0000
Nerves	0.0261
Kidney t	0.0000
Ovary uterus	0.0068
Prostate n	0.0243
Sensory organs	0.0000
White blood cells	0.0000

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0000	0.0023	0.0000	undef
Breast	0.0035	0.0014	2.5048	0.3992
Large intestine	0.0019	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0024	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Brain	0.0041	0.0020	2.0309	0.4924
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0010	0.0137	0.0738	13.5431
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0037	0.9278	1.0778
Kidney	0.0022	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0057	0.0039	1.4470	0.6911
T lymphoma	0.0126	0.0000	undef	0.0000
Uterus	0.0015	0.0000	undef	0.0000
White blood cells	0.0062	0.0000	undef	0.0000
Hematopoietic	0.0027	0.0000	undef	0.0000
Penis	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

STANDARDIZED/SUBTRACTED LIBRARIES
0.0000 % frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0058
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0040
Kidney t	0.0000
Ovary Uterus	0.0180
Prostate n	0.0485
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 241

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0000	undef	undef
Breast	0.0070	0.0098	0.7157	1.3973
Large intestine	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0320	0.0000	undef
Ovary	0.0030	0.0024	1.2443	0.8036
Endocrine tissue	0.0032	0.0000	undef	0.0000
Brain	0.0012	0.0199	0.0580	17.2337
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0061	0.0000	undef	0.0000
Testicles	0.0080	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0064	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0045	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
T lymphoma	0.0085	0.0052	1.6279	0.6143
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0103	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Seminal vesicle	0.0107			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0040
Ovary uterus	0.0000
Prostate n	0.0180
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 242

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0047	0.0000	undef
Breast	0.0018	0.0028	0.6262	1.5969
Large intestine	0.0057	0.0028	2.0184	0.4955
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0048	0.0035	1.3580	0.7364
Brain	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0030	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0128	0.0000	undef
Kidney	0.0034	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
T lymphoma	0.0057	0.0026	2.1706	0.4607
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0030	0.0046	0.6426	1.5563
Hematopoietic	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0030
Kidney t	0.0000
Ovary uterus	0.0045
Prostate n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 243

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0000	undef	undef
Breast	0.0026	0.0014	1.8786	0.5323
Large intestine	0.0038	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0059	0.0000	undef	0.0000
Endocrine tissue	0.0032	0.0071	0.4527	2.2091
Brain	0.0012	0.0090	0.1289	7.7552
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0029	0.0018	1.5786	0.6335
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
T lymphoma	0.0047	0.0013	3.6176	0.2764
Uterus	0.0025	0.0000	undef	0.0000
White blood cells	0.0030	0.0092	0.3213	3.1125
Hematopoietic	0.0021	0.0000	undef	0.0000
Penis	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0020
Kidney t	0.0000
Ovary Uterus	0.0180
Prostate n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 244

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0117	0.0117	0.9957 1.0043
Breast	0.0097	0.0070	1.3777 0.7259
Large intestine	0.0077	0.0000	undef 0.0000
Small intestine	0.0165	0.0000	undef 0.0000
Ovary	0.0000	0.0048	0.0000 undef
Endocrine tissue	0.0080	0.0071	1.1317 0.8836
Brain	0.0075	0.0080	0.9429 1.0605
Skin	0.0000	0.0000	undef undef
Hepatic	0.0046	0.0063	0.7324 1.3653
Heart	0.0071	0.0000	undef 0.0000
Testicles	0.0120	0.0059	2.0357 0.4912
Lung	0.0049	0.0000	undef 0.0000
Stomach-esophagus	0.0072	0.0000	undef 0.0000
Muscle-skeleton	0.0171	0.0111	1.5463 0.6467
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0050	0.0166	0.2992 3.3427
Prostate	0.0198	0.0078	2.5323 0.3949
T lymphoma	0.0051	0.0149	0.3381 2.9576
Uterus	0.0163	0.0046	3.5341 0.2830
White blood cells	0.0123	0.0000	undef 0.0000
Hematopoietic	0.0053		
Penis	0.0054		
Seminal vesicle	0.0141		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0245
Fetal	0.0081
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0259
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0020
Kidney t	0.0000
Ovary uterus	0.0090
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 245

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	under	undef
Bladder	0.0117	0.0117	0.9957	1.0043
Breast	0.0132	0.0084	1.5655	0.6388
Large intestine	0.0134	0.0028	4.7095	0.2123
Small intestine	0.0027	0.0107	0.2577	3.8812
Ovary	0.0030	0.0072	0.4148	2.4109
Endocrine tissue	0.0032	0.0106	0.3018	3.3136
Brain	0.0156	0.0070	2.2381	0.4468
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0093	0.0000	undef	0.0000
Heart	0.0122	0.0000	undef	0.0000
Testicles	0.0080	0.0000	undef	0.0000
Lung	0.0117	0.0037	3.1573	0.3167
Stomach-esophagus	0.0145	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.0000	undef	0.0000
Kidney	0.0045	0.0048	0.9285	1.0770
Pancreas	0.0033	0.0110	0.2992	3.3427
Prostate	0.0207	0.0000	undef	0.0000
T lymphoma	0.0025	0.0075	0.3381	2.9576
Uterus	0.0089	0.0138	0.6426	1.5563
White blood cells	0.0055	0.0607	0.0902	11.0896
Hematopoietic	0.0000			
Penis	0.0134			
Seminal vesicle	0.0000			
Sensory organs	0.0235			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0098
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0080
Kidney_t	0.0000
Ovary Uterus	0.0135
Prostate_n	0.0061
Sensory organs	0.0387
White blood cells	0.0000

Electronic Northern for Seq. ID: 246

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0141	0.0000	undef
Breast	0.0000	0.0042	0.0000	undef
Large intestine	0.0115	0.0028	4.0367	0.2477
Small intestine	0.0082	0.0000	undef	0.0000
Ovary	0.0000	0.0024	0.0000	undef
Endocrine tissue	0.0048	0.0053	0.9054	1.1045
Brain	0.0064	0.0030	2.1276	0.4700
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0046	0.0000	undef	0.0000
Heart	0.0051	0.0000	undef	0.0000
Testicles	0.0161	0.0059	2.7142	0.3684
Lung	0.0058	0.0074	0.7893	1.2669
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0037	1.3917	0.7186
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0055	0.2992	3.3427
Prostate	0.0057	0.0026	2.1706	0.4607
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0044	0.0000	undef	0.0000
White blood cells	0.0014	0.0000	undef	0.0000
Hematopoietic	0.0000			
Penis	0.0107			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0188
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0195
Nerves	0.0000
Kidney t	0.0050
Ovary Uterus	0.0000
Prostate n	0.0068
Sensory organs	0.0182
White blood cells	0.0000
	0.0000

G E N E S I S

Electronic Northern for Seq. ID: 247

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0136	0.1840 5.4361
Bladder	0.0039	0.0023	1.6595 0.6026
Breast	0.0106	0.0056	1.8786 0.5323
Large intestine	0.0096	0.0142	0.6728 1.4864
Small intestine	0.0027	0.0000	undef 0.0000
Ovary	0.0030	0.0048	0.6222 1.6073
Endocrine tissue	0.0016	0.0231	0.0696 14.3590
Brain	0.0139	0.0040	3.4816 0.2872
Skin	0.0000	0.0000	undef undef
Hepatic	0.0093	0.0127	0.7324 1.3653
Heart	0.0081	0.0275	0.2954 3.3858
Testicles	0.0000	0.0118	0.0000 undef
Lung	0.0078	0.0092	0.8419 1.1877
Stomach-esophagus	0.0072	0.0128	0.5668 1.7644
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidney	0.0112	0.0145	0.7737 1.2924
Pancreas	0.0066	0.0000	undef 0.0000
Prostate	0.0113	0.0065	1.7364 0.5759
T lymphoma	0.0152	0.0224	0.6762 1.4788
Uterus	0.0059	0.0000	undef 0.0000
White blood cells	0.0096	0.0607	0.1578 6.3369
Hematopoietic	0.0094		
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0071
Lung	0.0036
Adrenal gland	0.0254
Kidney	0.0371
Placenta	0.0061
Prostate	0.0249
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0156
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0181
Kidney t	0.0000
Ovary uterus	0.0180
Prostate n	0.0121
Sensory organs	0.0232
White blood cells	0.0000

2.2. Fisher Test

In order to decide whether a partial sequence S of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to S . If the null hypothesis can be rejected with high enough certainty, the gene belonging to S is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

Example 3

Automatic lengthening of the partial sequence

Automatic lengthening of partial sequence S is completed in three steps:

1. Determination of all sequences homologous to S from the total set of available sequences using BLAST.
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K.F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence C from the assembled sequences.

The consensus sequence C will generally be longer than initial sequence S . Its electronic Northern Blot will

accordingly deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences C_i (i: iteration index) obtained each time until the alternative hypothesis is rejected (if H_0 Exit; truncation criterion I) or until automatic lengthening is no longer possible (while $C_i > C_{i-1}$; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above described examples, it was possible to find the nucleic acid sequences described in Table I from prostate tumor tissue.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORFs) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

Example 4

Mapping of nucleic acid sequences on the human genome

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server (http://www.stanford.edu/RH/rhserver_form2.html). This program determines the STS marker which is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the gap between genome mapping and genome sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence mapping by electronic PCR. Genome Res. 7; 541-550). The database used here no longer corresponds to the one cited in the literature, but is a development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/index.html>). Analogously to the mapping by the hybrid panels, the results were

evaluated with the aforementioned software and the software of the Whitehead Institute (<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

Example 5

Obtaining genomic DNA sequences (BAC clones)

The genomic BAC clones containing the corresponding cDNAs (<http://www.tree.caltech.edu/>; Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797) were isolated with the procedure of "down-to-the-well". In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is moved into a certain raster, so that the DNA of these clones with a specific PCR can be studied. In doing so, "pooling" of the DNA of different BAC clones takes place. Combinatorial analysis makes it possible to determine the clones that contain the desired DNA. By fixing the clones, the address of the clones in the library can be determined. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

Seq.ID No.	Identified BACs		
3	320-L-23		
4	461-O-11		
8	283-P-15	322-B-7	317-H-19
24	272-N-9	340-L-19	554-D-3
31	293-K-21	337-I-17	363-J-15
46	410-A-9		
47	268-B-2	532-B-10	

Table 1

Col. 1 - Seq ID
 Col. 2 - Expression
 Col. 3 - Function
 Col. 4 - Modules
 Col. 5 - Cytogenetic localization
 Col. 6 - Nearest marker
 Col. 7 - Length of initial EST in bases
 Col. 8 - Length of claimed sequence in bases
 Col. 9 - Seq ID of initial sequence

Tabelle 1

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
2	im normalen Prostatagewebe erhöht	ZYXIN 2	LIM	7q33-7q35	D7S661	202	1437	
3	in gesundem Prostata- und Brustgewebe erhöht	Unbekannt		17p13.3	D17S2199-D17S1548	207	707	
4	im normalen Prostatagewebe erhöht	PCCMT		1p36.31	D1S2145-D1S2132	215	1265	
6	im normalen Prostatagewebe erhöht	Unbekannt	UBIQUITIN_CONJUGAT_2	1q21.2	D1S3384-D1S305	225	1330	
7	im normalen Prostatagewebe erhöht	Unbekannt		11q11-q13.1	D11S4205-D11S4535	231	762	
8	im normalen Prostatagewebe erhöht	Humanes Homolog des TEGT-Proteins aus der Ratte		10q23.1	D10S551-D10S532	246	1228	
9	im normalen Blasen- und Prostatagewebe erhöht	SRP20	rrm	6p21.2	NIB1566-WI-4186	243	914	
10	4x stärker als im normalen Prostatagewebe	Muf1		1p33-p32.3	D1S1558-D1S232	315	1126	
12	im normalen Prostatagewebe erhöht	Unbekannt		7p21.3-7p14.1	D7S2363	219	538	
13	im normalen Prostatagewebe erhöht	Unbekannt		22q12.1 - 22q13.1	D22S1144	210	321	
14	ausschließlich in der normalen Prostata	E4BP4	B_ZIP	9q22.1-q22.2	D9S787	217	847	
16	stärker im normalen Brust- und Prostatagewebe als im entsprechenden Tumor	HUMANer PHOSPHOLEMMAN PRECURSOR		19q13.1		210	573	
17	verstärkt in der normalen Prostata, verglichen mit dem entsprechenden Tumorgewebe	Mögliches Humans Homolog zu S1R		12q13.13 - 12q14.1	D12S1700-D12S1601	244	486	

Table 1

Seq ID	Expression	Function
2	elevated in normal prostate tissue	ZYXIN 2
3	elevated in healthy prostate and breast tissue	Unknown
5	elevated in normal prostate tissue	PCCMT
6	elevated in normal prostate tissue	Unknown
7	elevated in normal prostate tissue	Unknown
8	elevated in normal prostate tissue	Human homolog of TEGT protein from rats
9	elevated in normal bladder and prostate tissue	SRP20
10	4x more heavily than in normal prostate tissue	Muf1
12	elevated in normal prostate tissue	Unknown
13	elevated in normal prostate tissue	Unknown
14	solely in normal prostate	E4BP4
16	more heavily in normal breast and prostate tissue than in the corresponding tumor	HUMAN PHOSPHOLEMMAN PRECURSOR
17	intensified in normal prostate, compared to corresponding tumor tissue	Possible human homolog to S1R

UBIQUITIN_CONJUGAT_2 = UBIQUITIN_CONJUGATE_2

Seq ID	Expression	Function
18	about 6x more heavily in normal prostate compared to corresponding tumor tissue	Unknown
19	about 2x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
21	about 3x more heavily in normal prostate tissue than in corresponding tumor tissue, about 7x more often in breast and lung tumors than in corresponding normal tissue	Homolog to JANUS-A from <i>Drosophila melanogaster</i>
23	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
24	5x more heavily in normal prostate tissue than in corresponding tumor tissue, strongly expressed in skin tumors	E1F-6

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
18	ca. 6x stärker in der normalen Prostata, verglichen mit dem entsprechenden Tumorgewebe	Unbekannt		10q23.32 - 10q24.31	D10S551-D10S532	215	662	
19	ca. 2x stärker im normalen Prostata-gewebe als im entsprechenden Tumorgewebe	Unbekannt		2q35	D2S433-D2S295	225	750	
21	ca. 3x stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe, ca. 7x häufiger in Brust- und Lungentumoren als in entsprechenden Normalgeweben	Homolog zu JANUS-A aus <i>Drosophila melanogaster</i>		9q34.13	D9S158-D9S2053	229	1001	
23	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		1p36.13-p32.3	SGC32968	184	580	
24	5x stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe, stark exprimiert in Hauttumoren	E1F-6		20q11.1-q11.22		237	740	

Seq ID	Expression	Function
26	more heavily in normal prostate tissue than in corresponding tumor tissue	Homolog to HUMAN SORCIN
27	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
28	about 3x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
29	more heavily in normal prostate tissue than in corresponding tumor tissue	IL-6SAG
30	about 4x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
31	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
32	more heavily in normal prostate tissue than in corresponding tumor tissue, elevated 10x in muscle and skeletal tumors	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
26	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Homolog zu HUMANem SORCIN		1p36.11-p34.3	D1S233-D1S2548	219	975	
27	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		9p21.1-9q12	SHGC-7278-SHGC-33912	259	854	
28	ca. 3x stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		11q12.1 - 11q13.5	SHGC-15247-NIB715	288	802	
29	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	IL-6SAG		20p11.23-p11.21	D20S807-SHGC-11944	224	807	
30	ca. 4x stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		Xp11.23-p11.21	WI-5587-WI-5717	276	777	
31	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt				238	501	
32	stärker im normalen Prostatagewebe als im entsprechenden Tumorgewebe, 10x erhöht in Muskel- und Skelettumoren	Unbekannt		3p21.1 - 3p22.2	WI-9590-WI-3521	284	1104	

Seq. ID	Expression	Function
33	elevated in normal prostate tissue	Human homolog of WW-domain binding protein 1 from mice
35	elevated in normal prostate tissue and in gastrointestinal tumors	Unknown
36	elevated in normal prostate tissue	Id1
37	elevated in normal prostate tissue	Unknown
39	elevated in prostate tumors	C1 inhibitor
41	more heavily in normal prostate tissue than in corresponding tumor tissue	Acyl-protein thioesterase
42	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
43	about 6x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
33	in normalem Prostatagewebe erhöht	Humanes Homolog des WW-domain binding protein 1 aus der Maus		2p13.1	D2S145-SHGC-37085	208	810	
35	in normalem Prostatagewebe und in gastrointestinalen Tumoren erhöht	Unbekannt		3p23-p21.1	SHGC-32684-D3S4150	223	826	
36	in normalem Prostatagewebe erhöht	Id1	HLH	20p11.22 - 20q11.21	WI-1163	254	578	
37	in normalem Prostatagewebe erhöht	Unbekannt		8p12	SHGC-5722-SHGC-5765	293	799	
39	in Prostata Tumoren erhöht	C1 inhibitor	serpin	11p13-11q13.1	SHGC-30227-D11S1983	262	1743	
41	stärker in normalem Prostatagewebe als im entsprechenden Tumorgewebe	Acyl-protein thioesterase		6p21.31-q21.2	D6S1868-D6S1867	267	1183	
42	stärker in normalem Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		16q12.1-22.1	SHGC-6119-SHGC-15371	270	768	
43	ca. 6x stärker in normalem Prostata-gewebe als im entsprechenden Tumorgewebe	Unbekannt		17q11.2-q21.31	SHGC-30259-SHGC-13493	279	1029	

Seq. ID	Expression	Function
44	about 3x more heavily in normal prostate tissue than in corresponding tumor tissue, about 8x more often in a brain tumor than in comparable normal tissue	Unknown
46	elevated in normal prostate tissue	Unknown
47	elevated in normal prostatic, hepatic and ovarian tissue	Unknown
51	elevated in normal prostate tissue and hematopoietic tumors	Unknown
52	elevated in normal prostate tissue and in brain tumors	SPARC
53	elevated in normal prostate tissue	Unknown
54	elevated in normal prostate tissue and in skeletal tumors	Unknown
55	elevated in normal prostate tissue and hepatic tumors	B4-2

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
44	ca. 3x stärker in normalem Prostata-gewebe als im entsprechenden Tumorgewebe, ca. 8x häufiger im Gehirntumor als im vergleichbaren Normalgewebe	Unbekannt		16q23.1-q24.2	SHGC-32665-SHGC-11833	237	736	
46	in normalem Prostata-gewebe erhöht	Unbekannt		19p13.3	IB1264-WI-6480	259	1159	
47	in normalem prostatäischem, hepatischen und ovarial Gewebe erhöht	Unbekannt		6q13-q21		159	690	
51	in normalem Prostata-gewebe und in haematopoetischen Tumoren erhöht	Unbekannt		1p36.11	D1S3131-D1S2674	250	1186	
52	in normalem Prostata-gewebe und in Gehirntumoren erhöht	SPARC	kazal	5q21.1-q33.2	WI-7565-WI-6351	261	1029	
53	in normalem Prostata-gewebe erhöht	Unbekannt		15q23-24.1	D15S1241-D15S197	261	985	
54	in normalem Prostata-gewebe und in Skelettumoren erhöht	Unbekannt		4p14	D4S405-SHGC-9448	246	622	
55	in normalem Prostata-gewebe und hepatischen Tumoren erhöht	B4-2		6q16.2	D6S1644-D6S2057	239	1129	

Seq. ID	Expression	Function
58	about 3x more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
59	about 5x more heavily in normal prostate tissue than in corresponding tumor tissue	Methyl-CpG binding protein MBD2
60	more heavily in normal prostate tissue than in corresponding tumor tissue	Unknown
61	elevated in normal prostate tissue and in endocrine tumors	Unknown
62	elevated in normal prostate and breast tissue	Unknown
63	elevated in normal prostate, bladder and breast tumors	Unknown
64	expressed 1.8088x in benign prostate tissue	Homolog to RanBP7
217	expressed 2.894x in benign prostate tissue compared to the prostate tumor	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
58	ca. 3x stärker in normalem Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		1q12	SHGC-32015-D1S442	160	877	
59	ca. 5x stärker in normalem Prostatagewebe als im entsprechenden Tumorgewebe	Methyl-CpG bindendes Protein MBD2		18q21.32-18q21.32		288	1329	
60	stärker in normalem Prostatagewebe als im entsprechenden Tumorgewebe	Unbekannt		11q21-11q23.2		310	697	
61	in normalem Prostatagewebe und in endokrinen Tumoren erhöht	Unbekannt		17p11.2	AFMA126YD5	378	1389	
62	in normalem Prostata- und Brustgewebe erhöht	Unbekannt		4q21.21 - 4q21.23	WI-7565-WI-9200	260	535	
63	in normalem Prostata-, Blasen- und Brusttumoren erhöht	Unbekannt		16p12.3 - 16p13.11	AFMB354YF9	216	1098	
64	1.8088 x im gutartigen Prostatagewebe exprimiert	Homolog zu RanBP7		11p15.3-p15.5	D11S909-D11S4149	302	1860	
217	2.894 x im gutartigen Prostatagewebe gegenüber dem Prostatatumor exprimiert	Unbekannt	UBIQUITIN_CONJUGAT	1q21.2	D1S3384-D1S305		1880	6

Seq ID	Expression	Function
218	expressed 2.1705x in benign prostate tissue compared to the prostate tumor	Unknown
219	expressed 2.7494x in benign prostate tissue compared to the prostate tumor	Human homolog of TEGT from rats
220	expressed 2.46x in benign prostate tissue compared to the prostate tumor	TXBP151
221	expressed 1.7364x in benign prostate tissue compared to the prostate tumor	Possible human homolog to S1R
222	expressed 2.8941x in benign prostate tissue compared to the prostate tumor	Unknown
223	expressed 0.8348x in benign prostate tissue compared to the prostate tumor	Homolog to HYA22
224	expressed 1.0129x in benign prostate tissue compared to the prostate tumor	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
218	2.1705 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		11q11-q13.1	D11S4205-D11S4535		1024	7
219	2.7494 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Humanes Homolog des TEGT aus der Ratte		10q23.1	D10S551-D10S532		2383	8
220	2.46 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	TXBP151	COILS	7p21.3-7p14.1	D7S2363		3210	12
221	1.7364 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Mögliches Humans Homolog zu S1R		12q13.13 - 12q14.1	D12S1700-D12S1601		1030	17
222	2.8941 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		10q23.32 - 10q24.31	D10S551-D10S532		1216	18
223	0.8348 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Homolog zu HYA22		2q35	D2S433-D2S295		2369	19
224	1.0129 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		1p36.13-p32.3	SGC32968		849	23

Seq. ID	Expression	Function
225	expressed 8.6822x in benign prostate tissue compared to the prostate tumor	Homolog to HUMAN SORCIN
226	No similar sequence was found in the prostate tumor	Unknown
227	expressed 2.4117x in benign prostate tissue compared to the prostate tumor	IL-6SAG
228	expressed 2.1706x in benign prostate tissue compared to the prostate tumor	Unknown
229	No similar sequence was found in the prostate tumor	Unknown
230	expressed 1.447x in benign prostate tissue compared to the prostate tumor	Unknown
231	expressed 2.6529x in benign prostate tissue compared to the prostate tumor	Human homolog of WW-domain binding protein 1 from mice
232	expressed 3.1353x in benign prostate tissue compared to the prostate tumor	Homolog to OLIGOSACCHARYL TRANSFERASE STT3 subunit from C. elegans

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
225	8.6822 x im gutartigen Prostatagewebe gegenüber dem Prostatatumor exprimiert	Homolog zu HUMANem SORCIN	EF_HAND_2	1p36.11-p34.3	D1S233-D1S2548		1502	26
226	Es wurde keine ähnliche Sequenz im Prostatatumor gefunden	Unbekannt		9p21.1-9q12	SHGC-7278-SHGC-33912		1892	27
227	2.4117 x im gutartigen Prostatagewebe gegenüber dem Prostatatumor exprimiert	IL-6SAG		20p11.23-p11.21	D20S807-SHGC-11944		1522	29
228	2.1706 x im gutartigen Prostatagewebe gegenüber dem Prostatatumor exprimiert	Unbekannt		Xp11.23-p11.21	WI-5587-WI-5717		2016	30
229	Es wurde keine ähnliche Sequenz im Prostatatumor gefunden	Unbekannt					765	31
230	1.447 x im gutartigen Prostatagewebe gegenüber dem Prostatatumor exprimiert	Unbekannt		3p21.1 - 3p22.2	WI-9590-WI-3521		1611	32
231	2.6529 x im gutartigen Prostatagewebe gegenüber dem Prostatatumor exprimiert	Humanes Homolog des WW-domain binding protein 1 aus der Maus		2p13.1	D2S145-SHGC-37085		1473	33
232	3.1353 x im gutartigen Prostatagewebe gegenüber dem Prostatatumor exprimiert	Homolog zu der OLIGOSACCHARYL TRANSFERASE STT3 Untereinheit aus C. elegans		3p23-p21.1	SHGC-32684-D3S4150		2503	35

Seq. ID	Expression	Function
233	expressed 2.7132x in benign prostate tissue compared to the prostate tumor	Unknown
234	No similar sequence was found in the prostate tumor	Acyl-protein thioesterase
235	No similar sequence was found in the prostate tumor	Unknown
236	expressed 2.6529x in benign prostate tissue compared to the prostate tumor	Stat5b
237	expressed 3.2558x in benign prostate tissue compared to the prostate tumor	Unknown
236	expressed 4.3411x in benign prostate tissue compared to the prostate tumor	Unknown
239	expressed 3.1353x in benign prostate tissue compared to the prostate tumor	SDP3
240	expressed 1.447x in benign prostate tissue compared to the prostate tumor	Unknown

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
233	2.7132 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		8p12	SHGC-5722-SHGC-5765		1756	37
234	Es wurde keine ähnliche Sequenz im Prostata tumor gefunden	Acyl-protein thioesterase		6p21.31-q21.2	D6S1868-D6S1867		1286	41
235	Es wurde keine ähnliche Sequenz im Prostata tumor gefunden	Unbekannt		16q12.1-22.1	SHGC-6119-SHGC-15371		1230	42
236	2.6529 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Stat5b		17q11.2-q21.31	SHGC-30259-SHGC-13493		2328	43
237	3.2558 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		16q23.1-q24.2	SHGC-32665-SHGC-11833		1767	44
238	4.3411 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		19p13.3	IB1264-WI-6480		2311	46
239	3.1353 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	SDP3	PX	6q13-q21			1772	47
240	1.447 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		1p36.11	D1S3131-D1S2674		2409	51

Seq ID	Expression	Function
241	expressed 1.6279x in benign prostate tissue compared to the prostate tumor	Unknown
242	expressed 2.1706x in benign prostate tissue compared to the prostate tumor	Unknown
243	expressed 3.6176x in benign prostate tissue compared to the prostate tumor	Unknown
244	expressed 2.5323x in benign prostate tissue compared to the prostate tumor	Unknown
245	No similar sequence was found in the prostate tumor	LIMP II
246	expressed 2.1706x in benign prostate tissue compared to the prostate tumor	Unknown
247	expressed 1.7364x in benign prostate tissue compared to the prostate tumor	Homolog to RanBP7

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	Nächster Marker	Länge des Ausgangs-EST in Basen	Länge der beanspruchten Sequenz in Basen	Seq ID der Ausgangssequenz
241	1.6279 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		15q23-24.1	D15S1241-D15S197		2594	53
242	2.1706 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		4p14	D4S405-SHGC-9448		1012	54
243	3.6176 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		1q12	SHGC-32015-D1S442		1206	58
244	2.5323 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		17p11.2	AFMA126YD5		2514	61
245	Es wurde kein ähnliche Sequenz im Prostata tumor gefunden	LIMP II	CD36	4q21.21 - 4q21.23	WI-7565-WI-9200		3903	62
246	2.1706 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Unbekannt		16p12.3 - 16p13.11	AFMB354YF9		1730	63
247	1.7364 x im gutartigen Prostatagewebe gegenüber dem Prostata tumor exprimiert	Homolog zu RanBP7		11p15.3-p15.5	D11S909-D11S4149		3439	64

Table 2

DNA Sequence ORF Sequence ID No.
ID No.

2	66								
3	67	68	69	70					
4	71								
6	73								
7	74								
8	75								
9	82								
10	83								
12	90								
14	91								
16	92								
17	93								
18	97	98	99	100	101				
19	102	103	104	105					
21	109								
23	111	112	113						
24	114								
26	116								
27	117	118	119						
28	120	121	122	123	124				
29	128								
30	129	130	131						
31	132								
32	133								
33	134	135	136	137					
35	139	140	141	142	143	144	145	146	
36	147	148	149						
39	152								
41	154	155	156	157					
42	158	159	160	161					
43	162	163	164						
44	165								
46	168	169	170	171	172				
47	173								
51	183	184	185	186	187				
52	188	189	190	191	192	193			
54	194								
55	195								
58	201								
59	202	203	204	205	206				
60	207	208	209						
61	210								
62	214	215	216						
217	248								
218	249	250							
219	251								
220	252								
221	253								

<u>DNA Sequence</u>	<u>ORF Sequence</u>
<u>ID No.</u>	<u>ID No.</u>

222	254 255
223	256
224	257
225	258
226	259 260
227	261 262
228	263
229	264 265
230	266
231	267 268
232	269
233	270 271
234	272 273
235	274 275
236	276 277
237	278 279
238	280 281
239	282
240	283 284
241	285 286
242	287 288
243	289 290
244	291 292
245	293
246	294
247	295

The inventive nucleic acid sequences Seq. ID No. 2-4, 6-10, 12-14, 16-19, 21, 23, 24, 26-33, 35-37, 39, 41-44, 46, 47, 49, 51-55, 58-64 and Seq. ID No. 217-247 of the determined candidate genes and the determined amino acid sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 are described in the following sequence protocol.

Sequence protocol**(1) GENERAL INFORMATION:****(i) APPLICANT**

- (A) NAME: metaGen - Gesellschaft fuer Genomforschung mbH
- (B) STREET: Ihnestrassse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP) D-14195
- (G) TELEPHONE: (030)-8413 1672
- (H) FAX: (030)-8413 1671

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Prostate Tissue

(iii) Number of sequences: 216

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0 version #1.25 (EPO)

(2) INFORMATION ON SEQ ID NO. 2:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1437 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

CTCCTTGGAA GTCCCCTTCC AGCTCCCAGC CTCTGCCCCA GGTTCCGGCT CCGGCTCAGA 60
GCCAGACACA GTTCCATGTT CAGCCCCAGC CCCAGCCCCA GCCTCAGGTC CAACTCCATG 120
TCCAGTCCCA GACCCAGCCT GTGTCTTTGG CTAACACCCA GCCCCGAGGG CCCCCAGCCT 180
CATCTCCGGC TCCAGCCCCCT AAGTTTTCTC CAGTGA CTCC TAAGTTTACT CCTGTGGCTT 240
CCAAGTTCAG TCCTGGAGCC CCAGGTGGAT CTGGGTCACA ACCAAATCAA AAATTGGGGC 300
ACCCCGAAGC TCTTTCTGCT GGCACAGGCT CCCCTCAACC TCCCAGCTTC ACCTATGCCC 360
AGCAGAGGGA GAAGCCCCGA GTGCAGGAGA AGCAGACCCC CGTGCCCCCA CCGGCTCAGA 420
ACCAAAACCA GGTGCGCTCC CCTGGGGCCC CAGGGCCCCCT GACTCTGAAG GAGGTGGAGG 480
AGCTGGAGCA GCTGACCCAG CAGCTAATGC AGGACATGGA GCATCCTCAG AGGCAGAATG 540
TGGCTGTCAA CGAACTCTGC GGCCGATGCC ATCAACCCCT GGCCCGGGCG CAGCAGCCGT 600
CCGCGCTCTA GGGCAGCTGT TCCACATCGC CTGCTTCACC TGCCACCACT GTGCGCAGAG 660
CTCCAGGGCC AGCAGTTCTA TCTCTGGAG GGGGCGCCGT ACTGCGAGGG CTGTTACACT 720
GACACCCTGG AGAAGTGTA TCGCGGG GAGCCCATCA CTGACCGCAT GCTGAGGGCC 780
ACGGGCAAGG CCTATCACCC GCACTGCTTC ACCTGTGTGG TCTGCGCCCG CCCCTGGAG 840
GGCACCTCCT TCATCGTGGA CCAGGCCAAC CGGCCCACT GTGTCCCCGA CTACCACAAG 900
CAGTACGCCC CGAGGTGCTC CGTCTGCTCT GAGCCCATCA TGCCTGAGCC TGGCCGAGAT 960
GAGACTGTGC GAGTGGTCGC CCTGGACAAG AACTTCCACA TGAAGTGTTA CAAGTGTGAG1020
GACTGCGGGA AGCCCCTGTC GATTGAGGCA GATGACAATG GCTGCTTCCC CCTGGACGGT1080
CACGTGCTCT GTCGGAAGTG CCACACTGCT AGAGCCCAGA CCTGAGTGAG GACAGGCCCT1140
CTTCAGACCG CAGTCCATGC CCCATTGTGG ACCACCCACA CTGAGACCAC CTGCCCCCAC1200
CTCAGTTATT GTTTTGATGT CTAGCCCCTC CCATTTCCAA CCCCTCCCTA GCATCCCAGG1260
TGCCCTGACC CAGGACCCAA CATGGTCTAG GGATGCAGGA TCCCCGCCCT GGGGTCTGGT1320
CCTCGCCCAT CCTGCAGGGA TTGCCACCG TCTTCCAGAC ACCCCACCTG AGGGGGGCAC1380
AAGGTTTAGT GCTGCTGCTT TCACTGCTGC ACCCGCGCCC TCGGCCGGCC CCCCAG 1437

```

(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 707 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGCGGCCCCG	GCCTTAAAGC	GTCCATTTC	CAGCGGCCCT	CCGCTGCGAG	ACCGCAGCCC	60
TTCTCTGGAG	TCTCAGAGCC	GCAAGACACC	ACGACTCCCA	GAGGACCTTG	CGTCGGGCAA	120
GAAAGACTAC	ACCTTCCAGA	GGCCTCTGCG	GCGCCGCGAC	AGGAAGCGGC	GGGCGAGCCG	180
AGTGTCTTG	CGCGTGGATC	CGAGCGACCA	TGGTGGCCCG	GGTGTGGTCG	CTGATGAGGT	240
TCCTCATCAA	GGGAAGTGTG	GCTGGGGGCG	CCGTCTACCT	GGTGTACGAC	CAGGAGCTGC	300
TGGGGCCCCAG	CGACAAGAGC	CAGGCAGCCC	TACAGAAGGC	TGGGGAGGTG	GTCCCCCCCCG	360
CCATGTACCA	GTTTCAGCCAG	TACGTGTGTC	AGCAGACAGG	CCTGCAGATA	CCCCAGCTCC	420
CAGCCCCTCC	AAAGATTTAC	TTTCCCATCC	GTGACTCCTG	GAATGCAGGC	ATCATGACGG	480
TGATGTCAGC	TCTGTCGGTG	GCCCCCTCCA	AGGCCCGCGA	GTACTCCAAG	GAGGGCTGGG	540
AGTATGTGAA	GGCGCGCACC	AAGTAGCGAG	TCAGCAGGGC	CGCCTGCCCC	GGCCAGAACG	600
GGCAGGGCTG	CCACTGACCT	GAAGACTCCG	GACTGGGACC	CCACTCCGAG	GGCAGGCCTC	660
CCGATTGCCG	GCCCAATAAA	GGACTTCAGA	AGTGAAAAAA	AAAAAAA		707

(2) INFORMATION ON SEQ ID NO. 4:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

CACTGGGATG GGCATACACT ACTCACAGGG TGTGTGAGAT GAGAAGAACA CGTCAANGTT 60
TTTATACTCA GATGTGGGAG CGACATCAAT GAAATCTGTA CTGTATGAAA GCTACACAAA 120
AATGGGCAGA CATTGTTTGA ATTGTGCCAG ATACCTAAAA TGTATGTTCA GAAAAGCATT 180
TTATCAACTC AGAAATATGA CTTATTTCTA GATTTCATGG CTTAATGAAT TTTTTCATTG 240
TTATATATAC CAAAGAGGCT TACGGGTTCA TTGATTGGTT TGAAAACCAG ACAGACGGCC 300
GTGAGCCACC ACGCCCAGCC AAGATGAACT CCTTAAGGAC AGGATTTGGT AAGTGATTGA 360
CTTCTTTTTT GTTCCATGAT CTTGAGATTA TTTTtagctt TATAAATTTA GCAGTGGCAG 420
GGCCCGTGGA GAATCAGGTT AATGAGGTAA AGGCTTCTG GGTATTTGCT GCCAAGGCCA 480
CATCACCAAT TTTCTCGATT TAAAAAAGT TCAAGAGATT TATTTTCCA TTGCAGGTTT 540
TAAAGTGGAG ATTCTGAAGT GGAAAATAGG TACTGTGAGA ACAAAGCTAC CTGGAAACAG 600
CATAGAGTGA AGCCTTTCGT GAGGGCTTGC AGGCCGCTGC TGAGTGGCAG TTTACAGAAG 660
AGGTCGCGGG GTGAGCCTCT TAGCAGGACA GAAAACAAGG CAGCAGCGCA CCTGCCACCC 720

CTTCACGAGC TGCTCCTTGA GCCTAAAAAG TAGGCTTTAT TCATCCCTTC TGTTCATTTA 780
CCAACCTGGG GGATTGATAC GACCGGGGAA AATGTTCCCTA AACCAGGAAG CTGCGTTAGC 840
GAATCAGCTT TGGTAAGATC TCGCCAACAG CTAGCTGCTT AGGAGTACCC CCACGATACG 900
CACAGCACAC CACTGTCCCT TCACTGCACT TTCTTCCTGC CTTAGGTAGT TGGGCTTGCC 960
ACCCTAGTTT GCTTTTGTAG TGGTTTGGCA AGGTTAGAAG GCCTCGGCCC CCTCTGTCAT1020
GCTGGGAAGT GCCTACTCTC TGGGCCACTG CTGCAGAGGC CGTGGCACTT GTCATGGGTT1080
TGGAAGACCC AGCCATCTGC AGCAGAGGCA GCCTATCCCA TTGCAAGGAG AGGAACTGAA1140
CGGAGTAATT ATTCTACTCT TCTTTTACA TAAATGGTTT AATTAAATA ATTCAAATT1200
TGGAATTTCC TTTCACAGAT ACTGATAATC CTTTCCAGTT CTAAATAAA AACTGCACTT1260
GGATT

```

(2) INFORMATION ON SEQ ID NO. 6:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1330 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

CTTGGAGAGG CTGGTGGACA TAAAGAAAGG GAATACTCTG CTATTGCAGC ATCTGAAGAG 60
GATCATCTCC GACCTGTGTA AACTCTATAA CCTCCCTCAG CATCCAGATG TGGAGATGCT 120
GGATCAACCC TTGCCAGCAG AGCAGTGCAC ACAGGAAGAC GTGTCTTCAG AAGATGAAGA 180
TGAGGAGATG CCTGAGGACA CAGAAGACTT AGATCACTAT GAAATGAAAG AGGAAGAGCC 240
AGCTGAGGGC AAGAAATCTG AAGATGATGG CATTGGAAAA GAAAACTTGG CCATCCTAGA 300
GAAAATTAAA AAGAACCAGA GGCAAGATTA CTTAAATGGT GCAGTGTCTG GCTCGGTGCA 360
GGCCACTGAC CGGCTGATGA AGGAGCTCAG GGATATATAC CGATCACAGA GTTTCAAAGG 420
CGGAAACTAT GCAGTCGAAC TCGTGAATGA CAGTCTGTAT GATTGGAATG TCAAACCTCT 480
CAAAGTTGAC CAGGACAGCG CTTTGCACAA CGATCTCCAG ATCCTCAAAG AGAAAGAAGG 540
AGCCGACTTC ATTCTACTTA ACTTTTCCTT TAAAGATAAC TTTCCCTTTG ACCCACCATT 600
TGTCAGGGTT GTGTCTCCAG TCCTCTCTGG AGGGTATGTT CTGGGCGGAG GGGCCATCTG 660
CATGGAACCT CTCACCAAAC AGGGCTGGAG CAGTGCCTAC TCCATAGAGT CAGTGATCAT 720
GCAGATCAGT GCCACACTGG TGAAGGGGAA AGCACGAGTG CAGTTTGGAG CCAACAAATC 780
TCAATACAGT CTGACAAGAG CACAGCAGTC CTACAAGTCC TTGGTGCAGA TCCACGAAAA 840
AAACGGCTGG TACACACCCC CAAAAGAAGA CGGCTAACCC TGGAGTATCA CCCTTCCTCC 900
CTCCCCAGGC ACCACTGGAC CAATTACCTT TGAATGCTGT ATTTGGATCT CACGCTGCCT 960
CTGTGGTTCC CTCCCTCATT TTTCTGGAC GTGATAGCTC TGCCTATTGC AGGACAATGA1020

TGGCTATTCT AAACGCTAAG GAAAAAAAAC AAACACAGAA CTGTTTCAAG TACTCAAGAC1080
TGACTTACAG ACCAACCAAC CACCTTGCTG GAACCCTTGC TAGCAGGCAT TCTTATAAAA1140
GAAACTTTCT AGCCTCCTTA TATTGCTGGA AACTCAGCTG TGCTCCAGAC TAGAGCCTCC1200
TTACCTATGC TATGGATTTT TAATTTATTT TCTCTTATTT CATGTACACT GCTTTTTTTG1260
GTTACAGTGT ATGATGGATG TGTATGAAAA AAATGTATCT TTGGGAAAAC AATTACAGTT1320
TGTTAATTTG                                     1330

```

(2) INFORMATION ON SEQ ID NO. 7:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 762 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCGGTCGGTA	GTGCGGCGCT	GTTTAAAGAT	GGCGGCGGAG	GAACCTCAGC	AGCAGAAGCA	60
GGAGCCGCTG	GGCAGCGACT	CCGAAGGTGT	TAAGTGTCTG	GCCTATGATG	AAGCCATCAT	120
GGCTCAGCAG	GACCGAATTC	AGCAAGAGAT	TGCTGTGCAG	AACCCCTCTG	TGTCAGAGCG	180
GCTGGAGCTC	TCGGTCCTAT	ACAAGGAGTA	TGCTGAAGAT	GACAACATCT	ATCAACAGAA	240
GATCAAGGAC	CTCCACAAAA	AGTACTCGTA	CATCCGCAAG	ACCAGGCCTG	ACGGCAACTG	300
TTTCTATCGG	GCTTTCGGAT	TCTCCCACTT	GGAGGCACTG	CTGGATGACA	GCAAGGAGTT	360
GCAGCGGTTT	AAGGCTGTGT	CTGCCAAGAG	CAAGGAAGAC	CTGGTGTCCC	AGGGCTTCAC	420
TGAATTCACA	ATTGAGGATT	TCCACAACAC	GTTTCATGGAC	CTGATTGAGC	AGGTGGAGAA	480
GCAGACCTCT	GTCGCCGACC	TGCTGGCCTC	CTTCAATGAC	CAGAGCACCT	CCGACTACCT	540
TGTGGTCTAC	CTGCGGCTGC	TCACCTCGGG	CTACCTGCAG	CGCGAGAGCA	AGTTCTTCGA	600
GCACTTCATC	GAGGGTGGAC	GGACTGTCAA	GGAGTTCTGC	CAGCAGGAGG	TGGAGCCCAT	660
GTGCAAGGAG	AGCGACCACA	TCCACATCAT	TGCGCTGGCC	CAGGCCCTCA	GCGTGTCCAT	720
CCAGGTGGAG	TACATGGACC	GCGGCGAGGG	CGGCACCACC	AA		762

(2) INFORMATION ON SEQ ID NO. 8:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1228 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

GAAAAGTTTC TGAACATGGG TGCACCCCTG GGAGTGGGCC TGGGTCTCGT CTTTGTGTCC 60
TCCATTGGGA TCTATGTTTC TTCCACCTAC CCACCCGTGG CTGGGGCCAC TCTTTACTCA 120
GTGGCAATGT ACGGTGGATT AGTTCTTTTC AGCATGTTCC TTCTGTATGA TACCCAGAAA 180
GTAATCAAGC GTGCAGAAGT ATCACCAATG TATGGAGTTC AAAAATATGA TCCCATTAAAC 240
TCGATGCTGA GTATCTACAT GGATACATTA AATATATTTA TGCGAGTTGC AACTATGCTG 300
GCAACTGGAG GCAACAGAAA GAAATGAAGT GACTCAGCTT CTGGCTTCTC TGCTACATCA 360
AATATCTTGT TTAATGGGGC AGATATGCAT TAAATAGTTT GTACAAGCAG CTTTCGTTGA 420
AGTTTAGAAG ATAAGAAACA TGTCATCATA TTTAAATGTT CCGGTAATGT GATGCCTCAG 480
GTCTGCCTTT TTTTCTGGAG AATAAATGCA GTAATCCTCT CCCAAATAAG CACACACATT 540
TTCAATTCTC ATGTTTGAGT GATTTTAAAA TGTTTTGGTG AATGTGAAAA CTAAAGTTTG 600
TGTCATGAGA ATGTAAGTCT TTTTTCTACT TTAAAATTTA GTAGGTTTAC TGAGTAACTA 660
AAATTTAGCA AACCTGTGTT TGCATATTTT TTTGGAGTGC AGAATATTGT AATTAATGTC 720
ATAAGTGATT TGGAGCTTTG GTAAAGGGAC CAGAGAGAAG GAGTCACCTG CAGTCTTTTG 780
TTTTTTTAAA TACTTAGAAC TTAGCACTTG TGTTATTGAT TAGTGAGGAG CCAGTAAGAA 840
ACATCTGGGT ATTTGGAACG AAGTGGTCAT TGTTACATTC ATCTGCTGAA CTTAACAAAA 900
CTGTTTCATC TGAAACAGGC ACAGGTGATG CATTCTCCTG CTGTTGCTTC TCAGTGCTCT 960
CTTTCCAATA TAGATGTGGT CATGTTTGAC TTGTACAGAA TGTTAATCAT ACAGAGAATC1020
CTTGATGGAA TTATATATGT GTGTTTTACT TTTGAATGTT ACAAAAGGAA ATAACTTTAA1080
AACTATTCTC AAGAGAAAAT ATTCAAAGCA TGAAATATGT TGCTTTTTC AGAATACAAA1140
CAGTATACTC ATGAAAAAAA AATGTTTTTT TATTTTTCGA TATTTATTGA ACTGTCTAAT1200
TGAATACAGC TTGCTCTTGT CACCTCAA

```

(2) INFORMATION ON SEQ ID NO. 9:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 914 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

GGCGGTGGTC CGCCATTTTCG TGGACGCCGG GTGAGTGAGA GAGTTGGTTG GTGTTGGGCC 60
GGAGGAAAGC GGAAGACTC ATCGGAGCGT GTGGATTGA GCCGCCGCAT TTTTAAACCC 120
TAGATCTCGA AATGCATCGT GATTCCTGTC CATTGGACTG TAAGGTTTAT GTAGGCAATC 180
TTGGAACAA TGGCAACAAG ACGGAATTGG AACGGGCTTT TGGCTACTAT GGACCACTCC 240
GAAGTGTGTG GGTGCTAGA AACCCACCCG GCTTTGCTTT TGTTGAATTT GAAGATCCCC 300
GAGATGCAGC TGATGCAGTC CGAGAGCTAG ATGGAAGAAC ACTATGTGGC TGCCGTGTAA 360
GAGTGGAAC TCGAATGGT GAAAAAGAA GTAGAAATCG TGGCCACCT CCCTCTGGG 420
GTCGTCGCCC TCGAGATGAT TATCGTAGGA GGAGTCCTCC ACCTCGTCGC AGATCTCCAA 480
GAAGGAGAAG CTTCTCTCGC AGCCGGAGCA GGTCCCTTTC TAGAGATAGG AGAAGAGAGA 540
GATCGCTGTC TCGGGAGAGA AATCACAAGC CGTCCCGATC CTTCTCTAGG TCTCGTAGTC 600
GATCTAGGTC AAATGAAAGG AAATAGAAGA CAGTTTGCAA GAGAAGTGGT GTACAGGAAA 660
TTACTTCATT TGACAGGAGT ATGTACAGAA AATTCAAGTT TTGTTTGAGA CTTCATAAGC 720
TTGGTGCATT TTTAAGATGT TTTAGCTGTT CAAATCTGTT TGTCTCTTGA AACAGTGACA 780
CAAAGGTGTA ATTCTCTATG GTTTGAAATG GATCATACGA GGCATGTAAT ACCAAGAATT 840
GTTACTTTAC AATGTTCCCT TAAGCCAAAA TTGAATTGCT TTTGAACTTT TAGTTATGCA 900
CAGACTGATA ATAA 914

```

(2) INFORMATION ON SEQ ID NO. 10:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1126 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GAGGCAGCCC	TGACACTATG	CCACCTGCTG	AGCTCCTGGG	TGTCACTAGA	GAGCCTCACA	60
CTCTCCTACA	ATGGCCTGGG	CTCTAACATC	TTCCGCCTGC	TAGACAGCCT	GCGGGCCCTG	120
TCAGGCCAGG	CTGGATGTCG	CCTCCGTGCC	CTGCATCTCA	GTGACCTGTT	CTCACCCTG	180
CCCATCCTGG	AGCTGACACG	TGCTATCGTG	CGAGCACTGC	CCCTGCTACG	GGTCCTCTCT	240
ATTCGTGTTG	ACCACCCAAG	CCAGCGGGAC	AACCCTGGTG	TGCCAGGGAA	TGCAGGGCCC	300
CCTAGCCACA	TAATAGGCGA	TGAGGAGATA	CCAGAAAAC	GCCTGGAGCA	GTTGGAGATG	360
GGNATTTCCA	CGGGGAGCCC	AGCCAGCCCC	ACTGCTGTGC	TCCGTTCTGA	AGGCCTCGGG	420
TTCTCTGCAG	CAGCTGTCCC	TGGATAGTGC	CACCTTTGCC	TCTCCCCAGG	ATTTTGGGCT	480
TGTTTTGCAA	ACACTCAAAG	AGTACAACCT	AGCCCTGAAA	AGACTGAGCT	TCCATGACAT	540
GAATCTCGCT	GACTGTCAGA	GCGAGGTGCT	CTTTTTGCTA	CAGAATCTGA	CTCTGCAAGA	600
GATTACCTTC	TCCTTCTGCC	GTCTGTTTGA	GAAGCGCCCA	GCCCAATTTC	TGCCTGAGAT	660
GGTTGCTGCT	ATGCAAGGGCA	ACTCCACACT	GAAGGGCCTC	CGGCTGCCAG	GGAACCGCCT	720
GGGGAATGCT	GGCCTGCTGG	CCTTGGCAGA	TGTTTTCTCA	GAGGATTCAT	CCTCCTCTCT	780
CTGTCAGCTG	GACATCAGTT	CCAACATGAT	CAAGCCAGAT	GGGCTTCTGG	AGTTCGCCAA	840
GCGGCTGGAG	CGCTGGGGCC	GTGGAGCCTT	TGGTCCACTG	CGCCTCTTCC	AAAACCTGGT	900
GGACCAGGAT	GCAGTCACAG	CCAGGGAAGC	CATCCGGCGG	CTCCGGGCTA	CTGCCCATGT	960
GGTTAGCGAC	TCATGGGACT	CATCCCAGGC	CTTCGCAGAT	TATGTTAGCA	CCATGTGATG	1020
GGGCCCCGTAC	CTCACAGTCT	CATGCTCGGT	ACCATCAGCT	TGCAGGGGCT	GAAGCATGGG	1080
CTGCCCAGAA	CCCCAACCCAC	CAGTTCTATC	TTTCTCTTTC	TGTGAC		1126

(2) INFORMATION ON SEQ ID NO. 12:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 538 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TAGACCACTG	AGGAGACCAT	AGAGCGGATG	CTTTCATGCA	CCCTTTACTG	CACTTTCTGA	60
CCAGGAGCTA	CTTTGAGTTT	GGTGTTACTA	GGATCAGGGT	CAGTCTTTGG	CTTATCAATA	120
AATTTTAATC	TCTGTTAATC	TTACCTGCTT	TAAAAAAAAG	TTCTTGTTGTG	TTCGTATCTT	180
TATTTATTCC	CTAGTTTGCA	GAAGTGTCTG	AATAAAGGAT	ACAAGGATTA	TTTCAATGTT	240
ACTGCACTGA	AAAACGTGTA	TGTATTAGTG	TGCTAGATTA	TTTAGCAGAA	TATTCACAAG	300
TTTCTGTTGA	CCTTGTTGAT	TGAGCATGAC	TACTAAATAT	TATGTAATAA	AAAGCATTGT	360
TCATAACAGT	CTTATGAAGT	AGTTCTTCGA	ATATAGAAAG	TTCTATAAAT	TAGCCCATGA	420
AATGATAGGT	TTTTAATTTT	CAGAAATGGA	GCTGCATGTA	GAATGAGATC	ACATGCTTTT	480
ATATGTGAAA	TATTGGTTTT	AGCAATTAAC	AGAAGGCATA	CTTTGCTAAT	TTTATGGC	538

(2) INFORMATION ON SEQ ID NO. 13:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 321 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCCTACAAC	GGTTGCAAAC	TCAGGCTTTC	CCCAGTGACC	AACAATTTTA	ATTCCAAGAG	60
GTGAGGATCT	CAGGAGGTGG	CATTCACCCA	CCAGGGAGCT	AGGGAAAGGG	AACCAAGCTG	120
TCTCCACACC	CAGGAGAGGT	GTCCCTCCAG	CCAAGGCAGG	CAGGACACTC	TGCAGCTCTC	180
CCTCCTGTGC	CCAGGCCCTT	GACTACACTC	TCATCTGCCA	TCTGAGCTAA	GCCAGGAAGG	240
CAGTTAAAGA	AAGGCCCCCA	AACATGAAGC	AGGGACAAGG	AGACGGACAG	GGGTCAGATG	300
ACCCATTGAT	AGGGAAGAGA	G				321

(2) INFORMATION ON SEQ ID NO. 14:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 847 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

AGACAAATCT TCTGCATGTC GGAGGAACGG GAATTATTCT GATGAAAAGA AAGATGCTAT 60
GTATTGGGAA AAAAGGCGGA AAAATAATGA AGCTGCCAAA AGATCTCGTG AGAAGCGTCG 120
ACTGAATGAC CTGGTTTTAG AGAACAACT AATTGCAC TGAGAGAGAA ACGCCACTTT 180
AAAAGCTGAG CTGCTTTCAC TAAAATTAAA GTTTGGTTTA ATTAGCTCCA CAGCATATGC 240
TCAAGAGATT CAGAACTCA GTAATTCTAC AGCTGTGTAC TTCAAGATT ACCAGACTTC 300
CAAATCCAAT GTGAGTTCAT TTGTGGACGA GCACGAACCC TCGATGGTGT CAAGTAGTTG 360
TATTTCTGTC ATTAAACACT CTCCACAAAG CTCGCTGTCC GATGTTTCAG AAGTGTCTTC 420
AGTAGAACAC ACGCAGGAGA GCTCTGTGCA GGAAGCTGC AGAAGTCCTG AAAACAAGTT 480
CCAGATTATC AAGCAAGAGC CGATGGAATT AGAGAGCTAC ACAAGGGAGC CAAGAGATGA 540
CCGAGGCTCT TACACAGCGT CCATCTATCA AAATATATG GGAATTCTT TCTCTGGGTA 600
CTCACACTCT CCCCCACTAC TGCAAGTCAA CCGATCCTCC AGCAACTCCC CGAGAACGTC 660
GGAACTGAT GATGGTGTGG TAGGAAAGTC ATCTGATGGA GAAGACGAGC AACAGGTCCC 720
CAAGGGCCCC ATCCATTCTC CAGTTGAACT CAAGCATGTG CATGCAACTG TGGTTAAAGT 780
TCCAGAAGTG AATTCCTCTG CCTTGCCACA CAAGCTCCGG ATCAAAGCCA AAGCCATGCA 840
GATCAAA

```

(2) INFORMATION ON SEQ ID NO. 16:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 573 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGAGGCTGCT	GGGGGCGGCG	CGTCCAGCTC	TGGGCCAGGG	GGTCCAAAGT	GCTCAGCCCC	60
CGGGGCACAG	CAGGACGTTT	GGGGGCCTTC	TTTCAGCAGG	GGACAGCCCG	ATTGGGGACA	120
ATGGCGTCTC	TTGGCCACAT	CTTGGTTTTC	TGTGTGGGTC	TCCTCACCAT	GGCCAAGGCA	180
GAAAGTCCAA	AGGAACACGA	CCCGTTCAC	TACGACTACC	AGTCCCTGCA	GATCGGAGGC	240
CTCGTCATCG	CCGGGATCCT	CTTCATCCTG	GGCATCCTCA	TCGTGCTGAG	CAGAAGATGC	300
CGGTGCAAGT	TCAACCAGCA	GCAGAGGACT	GGGGAACCCG	ATGAAGAGGA	GGGAACCTTC	360
CGCAGCTCCA	TCCGCCGTCT	GTCCACCCGC	AGGCGGTTAG	AACACCTGGA	GCGATGGAAT	420
CCGGCCAGGA	CTCCCCTGGC	ACCTGACATC	TCCCACGCTC	CACCTGCGCG	CCCACGGGCC	480
CCTCCGCCGC	CCCTTCCCCA	GCCCTGCCCC	CGCAGACTCC	CCCTGCCGCC	AAGACTTCCA	540
ATAAAACGTG	CGTTCCTCTC	GACAAAAAAA	AAA			573

(2) INFORMATION ON SEQ ID NO. 17:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 486 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

GCCGCACGGC TTGCTGGGGC TGGGCTCTTC CTCGCGGAAG TGGGGAGGAG GCGGTTGCGG 60
TTAGTGGACC GGGACCGGTA GGGGTGCTGT TGCCATCATG GCTGACCCCG ACCCCCGGTA 120
CCCTCGCTCC TCGATCGAGG ACGACTTCAA CTATGGCAGC AGCGTGGCCT CCGCCACCGT 180
GCACATCCGA ATGGCCTTTC TGAGAAAAGT CTACAGCATT CTTTCTCTGC AGGTTCTCTT 240
AACTACAGTG ACTTCAACAG TTTTTTTATA CTTTGAGTCT GTACGGACAT TTGTACATGA 300
GAGTCCTGCC TTAATTTTGC TGTTTGCCCT CGGATCTCTG GGTTTGATTT TTGCGTTGAC 360
TTTAAACAGA CATAAGTATC CCCTTAACCT GTACCTACTT TTTGGATTGA CGCTGTTGGA 420
AGCTCTGACT GTGGCAGTTG TTGTTACTTC TATGATGTAT ATATTATCTG CAAGCTTTCA 480
TACTGA 486

```

(2) INFORMATION ON SEQ ID NO. 18:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 662 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

CTTTTTTCCT CTAATCCTTC CCCTTCACAC CCCCCTGGCT GGAAGGAACC TCGGCTTCCC 60
TGAAAGCTTG GGGGTCCAC CTTCTTACC CCACCCGGGA GGAACGCCCA GGGCCCCGGG 120
CTTGTTTCTC CTCTTGTTTT CTTTTGGGC AGTTTGATCA CTGATCGAGT AAGGAATGAC 180
CTTTAGATTG TCGGACTTTT GTTTTTGTTT TTTTAAATTT TTTTAAACCA AGAATGATTT 240
CTCCTGCTTC CTTCTCCTCA CCATCTTCCC AGACGGAGTT CAAAGGCCAC TTCTCAAGCA 300
GCTTTTGGCA CCTTCAGCCT CAGAGTGGAA TCTTTTAAAG ACAGGACCCC TATGTCCAGG 360
AAAGGGGAAA AGGAACCTTG CCAATGATAG TGACCACAGC AAAAGCAATA AAATAATAAA 420
ATAAAAAACA ATAGCACAGC CTTGTGTGAG GTCAGCAGG AGGAGGGGCT GCCCGGAGTT 480
GGGTCCTTGC CTGGATTTTG ACACAGCAAC TTCCTGTAGT GAGCACTTTG TATGAATCGT 540
GGACTTCCTG TTCTCAAGGC GCAGGTATTT ATTCTGTATC TGTCTAGAGC ACACACCAAA 600
ATCCAACCTT CTAATAAACA TGATGGCGCA GTCCCCAAAA AGGAAACAGA AGAAGAAAAG 660
GG 662

```

(2) INFORMATION ON SEQ ID NO. 19:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 750 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATAGATTTTG	AGGGGAAGGA	GAGAGGGAAG	GGTCAGGGTA	GAGACACCCC	TCCCTTGCCC	60
CTTTCCTGGG	CCCAGAAGTT	GGGGGGAGGG	AGGGAAAGGA	TTTTTACATT	TTTTAAACTG	120
CTATTTTCTG	AATGGAACAA	GCTGGGCCAA	GGGGCCCAGG	CCCTGTCTC	TGTCCCTCAC	180
ACCCCTTTGC	TCCGTTTATT	CATTCAAAAA	AACATTTCTT	GAGCACCTTC	TGTGCCCAGC	240
ATATGCTAGG	CCCACCAGCT	AAGTGTGTGT	GGGGGGTCTC	TACGCCAGCT	CATCAGTGCC	300
TCCTTGCCCA	TCCTTCACCG	GTGCCTTTGG	GGGATCTGTA	GGAGGTGGGA	CCTTCTGTGG	360
GGTTTGGGGA	TCTCCAGGAA	GCCCGACCAA	GCTGTCCCCT	TCCCCTGTGC	CAACCCATCT	420
CCTACAGCCC	CCTGCCTGAT	CCCCTGCTGG	CTGGGGGCGAG	CTCCCAGGAT	ATCCTGCCTT	480
CCAAGTGT	CTGAAGCCCC	TCCTCCTAAC	ATGGCGATTG	CGGAGGTCAA	GGCCTTGGGC	540
TCTCCCCAGG	GTCTAACGGT	TAAGGGGACC	CACATACCAG	TGCCAAGGGG	GATGTCAAGT	600
GGTGATGTCG	TTGTGCTCCC	CTCCCCCAGA	GCGGGTGGGC	GGGGGGTGAA	TATGGTTGGC	660
CTGCATCAGG	TGGCCTTCCC	ATTTAAGTGC	CTTCTCTGTG	ACTGAGAGCC	CTAGTGTGAT	720
GAGAACTAAA	GAGAAAGCCA	GACCCCTAAA				750

(2) INFORMATION ON SEQ ID NO. 21:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1001 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

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GGGGGAGAGA GGGAGGCCTT TGGCGGTGG GGGCCACGGG GAGGGTGGTC CTCGGACTAC 60
GTGCGGGACA GGAGGTCAGG GCTGGCAAGT CCCTCAGGCC TCCCTCGTTG CCCCAGCCTC 120
GCGGGCCGCC TAACTGCCCC GTTCCAAGGG TGCCACCGGA CCCCCTGGA GAGGAACTTC 180
TCCGTTGGCT GATTTCATCA CCACCCATTC CCGATTCCAC GTTTCCTTTA AGCGGGGCTG 240

GCGGAGCGCA AGGGGGCAAG GAACTGGATT GCGATTGGTC AGCACGTGCC TCGGTCGGCG 300
GTACAATTGG CTGAGGCGCT GGGCCTTGGG AAGCATTTCC CGACGGGATT GGTCTGTCGT 360
CTCGCAGAGC CCGCCTCCCG CAGTACAAGC GGCCCCCGGG TGGGGGGGGA GGAGGGGACT 420
CGGGGAGGAG GAACATGGCG GTGGCGGACC TCGCTCTCAT TCCTGATGTG GACATCGACT 480
CGGACGGCGT CTTCAAGTAT GTGCTGATCC GAGTCCACTC GGCTCCCCGC TCCGGGGGCTC 540
GGGCTGCAGA GAGCAAGGAG ATCGTGCGCG GCTACAAGTG GGCTGAGTAC CATGCGGACA 600
CTACGACAA AGTGTCGGGC GACATGCAGA AGCAAGGCTG CGACTGTGAG TGTCTGGGCG 660
GCGGGCGCAT CTCCCACCAG AGTCAGGACA AGAAGATTCA CGTGTACGGC TATTCCATGG 720
CTATGGTCC TGCCACGAC GGCATTTCAA CTGAGAAAAT CAAAGCCAAG TACCCCGACT 780
CGAGGTCAC CTGGGCTAAC GACGGCTACT GAGCACTCCC AGCCCGGGGC CTGCTGCCTC 840
CAGCAGCCAC TTCAGAGCCC CCGCCTTTGC CTGCACTCCT CTTGCAGGGC TGGCCCTGCC 900
TGCTCCTGCG GCAGCCTCTG GTGACGTGCT GTCCACCAGG CCTTGAGAC AGGCTAGCCT 960
GGCCACAGAA TTAAACGTGT TGCCACACCT GCCGGCTTCT G 1001

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(2) INFORMATION ON SEQ ID NO. 23:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 580 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CGAAACGTGC	GCAGGCGCCG	GCCGCTGCGC	TGCAGATGGC	GGAAATGGAT	CCGGTAGCCG	60
AGTTCCCCCA	GCCTCCCGGT	GCTGCGCGCT	GGGCTGAGGC	CCTTCTGCGA	TGTTTTACCT	120
GGCTGCGGCT	GTGTCAGATT	TCTATGTTCC	TGTCTCTGAA	ATGCCTGAAC	ACAAGATCCA	180
GTCATCTGGG	GGCCCACTGC	AGATAACAAT	GAAGATGGTG	CCAAACTGC	TTTCTCCTTT	240
GGTTAAAGAT	TGGGCTCCCA	AAGCATTTAT	AATTTCTTTT	AAGTTGGAGA	CTGACCCCGC	300
CATTGTAATT	AATCGAGCTC	GGAAGGCTTT	GGAAATTTAT	CAGCATCAAG	TGGTGGTGCC	360
TAATATCCTT	GAGTCACGAC	AGTCCTTTGT	GTTTATTGTA	ACCAAAGACT	CGGAAACCAA	420
GTTATTGCTA	TCAGAGGAAG	AAATAGAAAA	AGGCGTAGAG	ATAGAAGAGA	AGATAGTGGA	480
TAATCTTCAG	TCTCGACACA	CAGCTTTTAT	AGGTGACAGA	AACTGAAGTA	AAAAGCCCTT	540
ATAGGATCAA	AAATTGTTCA	GGGCTCTTAG	AGATGGTGAA			580

(2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 740 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GGATGCGTGG	CGGGGAGCGC	CGGGCTCTCC	CGGAAGTCTC	CCTGGACGGA	AGTGGAACG	60
GAAACCTTTT	TAGGGAGTCC	AAGGTACAGT	CGCCGCGTGC	GGAGTTGTTA	CTGGTTACTT	120
GGCCTCATGG	CGGTCCGAGC	TTCGTTCGAG	AACAACTGTG	AGATCGGCTG	CTTTGCCAAG	180
CTCACCAACA	CCTACTGTCT	GGTAGCGATC	GGAGGCTCAG	AGAACTTCTA	CAGTGTGTTC	240
GAGGGCGAGC	TCTCCGATAC	CATCCCCGTG	GTGCACGCGT	CTATCGCCGG	CTGCCGCATC	300
ATCGGGCGCA	TGTGTGTGGG	GAACAGGCAC	GGTCTCCTGG	TACCCAACAA	TACCACCGAC	360
CAGGAGCTGC	AACACATTCG	CAACAGCCTC	CCAGACACAG	TGCAGATTAG	GCGGGTGGAG	420
GAGCGGCTCT	CAGCCTTGGG	CAATGTCACC	ACCTGCAATG	ACTACGTGGC	CTTGGTCCAC	480
CCAGACTTGG	ACAGGGAGAC	AGAAGAAATT	CTGGCAGATG	TGCTCAAGGT	GGAAGTCTTC	540
AGACAGACAG	TGGCCGACCA	GGTGCTAGTA	GGAAGCTACT	GTGTCTTCAG	CAATCAGGGA	600
GGGCTGGTGC	ATCCCAAGAC	TTCAATTGAA	GACCAGGATG	AGTGTCTCTC	TTTTCAAGTC	660
CCTTGTTGCG	GGGATGTGAA	CGAAGCATTA	AGTGATTCTT	GGGATGTGTA	TAATGTGTCC	720
TTCGTGCCTG	AAACCACCA					740

(2) INFORMATION ON SEQ ID NO. 26:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 975 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ATGGGCTACA	ACCTGAGCCC	CCAGTTCACC	CAGCTTCTGG	TCTCCCGCTA	CTGCCCACGC	60
TCTGCCAATC	CTGCCATGCA	GCTTGACCGC	TTCATCCAGG	TGTGCACCCA	GCTGCAGGTG	120
CTGACAGAGG	CCTTCCGGGA	GAAGGACACA	GCTGTACAAG	GCAACATCCG	GCTCAGCTTC	180
GAGGACTTCG	TCACCATGAC	AGCTTCTCGG	ATGCTATGAC	CCAACCATCT	GTGGAGAGTG	240
GAGTGCACCA	GGGACCTTTC	CTGGCTTCTT	AGAGTGAGAG	AAGTATGTGG	ACATCTCTTC	300
TTTTTCCTGTC	CCTCTAGAAG	AACATTCTCC	CTTGCTTGAT	GCAACACTGT	TCCAAAAGAG	360
GGTGGAGAGT	CCTGCATCAT	AGCCACCAAA	TAGTGAGGAC	CGGGGCTGAG	GCCACACAGA	420
TAGGGGCCTG	ATGGAGGAGA	GGATAGAAGT	TGAATGTCCT	GATGGCCATG	AGCAGTTGAG	480
TGGCACAGCC	TGGCACCAGG	AGCAGGTCCT	TGTAATGGAG	TTAGTGTCCA	GTCAGCTGAG	540
CTCCACCCTG	ATGCCAGTGG	TGAGTGTTC	TCGGCCTGTT	ACCGTTAGTA	CCTGTGTTCC	600
CTCACCAGGC	CATCCTGTCA	AACGAGCCCA	TTTTCTCCAA	AGTGGAATCT	GACCAAGCAT	660
GAGAGAGATC	TGTCTATGGG	ACCAAGTGGCT	TGGATTCTGC	CACACCCATA	AATCCTTGTC	720
TGTTAACTTC	TAGCTGCCTG	GGGCTGGCCC	TGCTCAGACA	AATCTGCTCC	CTGGGCATCT	780
TTGGCCAGGC	TTCTGCCCTC	TGCAGCTGGG	ACCCCTCACT	TGCCTGCCAT	GCTCTGCTCG	840
GCTTCAGTCT	CCAGGAGACA	GTGGTCACCT	CTCCCTGCCA	ATACTTTTTT	TAATTTGCAT	900
TTTTTTTCAT	TTGGGGGCCAA	AAGTCCAGTG	AAATTGTAAG	CTTCAATAAA	AGGATGAAAC	960
TCTGGAAAAA	AAAAA					975

(2) INFORMATION ON SEQ ID NO. 27:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 854 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GAACACACAC	ACAGGTGTTT	TGACCAGCTC	AGGCTTGCCA	CAGTGAGCAA	CTCTGTGGCT	60
AGCAAAAGAG	AAGTTTATTT	GTGCCCAGCC	ATTGGTCACC	TTGGGTGATG	CACCAGATAG	120
CAGGCAGATG	TTGGTTCATT	GGCCTTCGTC	CTCTTTCCTC	CTAAAATAAT	ATTGGCTTTA	180
CCATCTTAAC	TCAGCTGTGG	GTTTTTTGTG	GTTTCTTGTT	TGTTTTTTGG	CATGAATTGT	240
CATCTTTGGT	GTTTTTTTAA	CCCCCAGCCC	CTCAAAAAAA	TAAGGCCTCC	AGGTATCAAG	300
ATCTCATATT	AGGATTTTCT	GTCCTTAATT	TTTTGAGCAA	AATCTGGAAA	ATGTGAAAGC	360
ATATTTAGAT	TTTATATACT	ATCTGAAATG	TGATTTGTTA	AGATTCTTAA	ATTTGGGCCT	420
CTTAGAATAA	TTTTGAATGA	GATCTACCGA	CTCACTTGTT	AGAATATTTT	TCACAGATTA	480
TCTTTGGGCC	TTTTCATTAG	AAAGCTGTTT	GTTTGTCCCC	CTGTTGGTAC	ATTTGGTTAC	540
CTCATTTTGC	CGTTTCAGAT	TGTGAAAGCT	CACAGGGGTG	TTTTTTGGAA	TCATTTGCTG	600
AGTCATTTTC	TCAAATCATA	TTCCATTGTA	TCAGTTAACA	TATAGTTTTA	AATGTATGTA	660
TTATAAATAT	CTGTAACCAA	ATCATTTGAA	GGCTTGATAA	ATTTTAAACA	AAGTTTGTAC	720
ATTTTTTTATG	AAAGTTACTA	GTAATGCTTT	ACTAAGTAGT	GCAATGAATT	TTTATTTTAA	780
ATCCCTGTGC	CCAATTTTGG	AGTTGAGAGG	GTTGTTGGTA	ATAAATGTAT	GATGTACACT	840
TAAAAA	AAAA					854

(2) INFORMATION ON SEQ ID NO. 28:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 802 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTTTTTTCAG	AGTGCTAGGG	CTTTATTACA	AATGGAGTTG	ACTGCTAGAG	AGGCCCTTCT	60
CCAATCTTTC	TTCTGTACCT	TCTTCCCTCC	CAAAGACATC	CCTCTAGGGG	AGGTCAGTAG	120
GCCATTAGGT	AGGAGGAAAT	CTGGAGAGTG	AAAAGGGGCC	TTGCTTTTGT	CAAAGTCCTC	180
TGAAACAACC	ACTGAGTCTG	AAGGCTGGCT	CCAGTTGAGA	ATCTTCTAGT	GGAAGAGGTT	240
TAGCTCTCAT	CTTCAAGGTC	CTTCATTTCT	ACATCCTGGG	GGGCTTTTGT	CTTCTTTTGC	300
CTTTTGAGCT	GTGGTTCACT	AGTCCTGGCT	GGCTTTGAAG	GGGCTTCCAC	TTCCATGGCT	360
GTCTTCTCTT	TCTGGGCAAG	CCGGATCTGC	TGGAGGAGTT	TTCTGCGCTT	CTTCCCTGAC	420
AGTGTAATGT	TGGCACGTGC	ACTGGACGCC	CGCTTCTTGA	GGTGGTGCCG	CGTGATCAGC	480
CCTTGGTCTA	TCACAGCCCC	GACCACCCGG	TGCCTCAGAC	GCCGCTCCCG	ATTCAACACC	540
CGCCGGCGTT	TGAACAGCTT	CTTCTTCAGC	TCCGTTCCGG	GCCGTTGAT	CTTCCCCCCC	600
GGAGCTCCCA	TAGTCGCGAT	TCCACTCCAG	TTCACGGTCC	GTACTTCCGC	TCAGCGCCGG	660
ATCCGCGGGC	TCCGCCCCGG	CCTTCCGCGG	GCCAATCGCA	ACTCGGGGGC	GGGTCCTCGG	720
GGTATATAAA	GGAGCTCCGC	GGTGCGGGAG	GCCTTTCGGA	GGGTGGTGAG	CTAGTAAGTG	780
TGGTTTTAGC	TGTAGTAGCC	AG				802

(2) INFORMATION ON SEQ ID NO. 29:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 807 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CCCCGTCCGC	GCGTGGTGGC	TGCTGCTGTG	CATGTCCCTG	CGATGGGAGT	CTTGTGCCCCA	60
GCCTGTCAGT	TTCCTCCCCA	GGGCAGAGCT	CCCCTTCCTG	CAAGAGTCTG	GGAGGCGGTG	120
CAGGCTGTCC	TGGCTGCTCT	GGGGAAGCCG	AGGGACAGCC	ATAACACCCC	CGGGACAGTA	180
GGTCTGGGCG	GCACCACTGG	GAACCTCTGA	CTTGAGTGTG	TTTGCCTCTT	CCTTGGGTAT	240
GAATGTGTGA	GTTCAACCCAG	AGGCCTGCTC	TCCTCACACA	TTGTGTGGTT	TGGGGTTAAT	300
GATGGAGGGA	GACACCTCCT	CATAGACGGC	AGGTGCCCAC	CTTTCAGGGA	GTCTCCCAGC	360
ATGGGCGGAT	GCCGGGCATG	AGCTGCTGTA	AACTATTTGT	GGCTGTGCTG	CTTGAGTGAC	420
GTCTCTGTCT	TGTGGGTGCC	AAGTGCTTGT	GTAAGAACTG	TGTTCTGAGC	CCCCTTTTCT	480
GGACACCAAC	TGTGTCCTGT	GAATGTATCG	CTACTGTGAG	CTGTTCCCGC	CTAGCCAGGG	540
CCATGTCTTA	GGTGCAGCTG	TGCCACGGGT	CAGCTGAGCC	ACAGTCCCAG	AACCAAGCTC	600
TCGGTGTCTC	GGGCCACCAT	CCGCCCACCT	CGGGCTGACC	CCACCTCCTC	CATGGACAGT	660
GTGAGCCCCG	GGCCGTGCAT	CCTGCTCAGT	GTGGCGTCAG	TGTCGGGGCT	GAGCCCCTTG	720
AGCTGCTTCA	GTGAATGTAC	AGTGCCCGGC	ACGAGCTGAA	CCTCATGTGT	TCCACTCCA	780
ATAAAAGGTT	GACAGGGAAA	AAAAAAA				807

(2) INFORMATION ON SEQ ID NO. 30:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 777 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

CTCTCTGCCA GCTGATGTGC CCTGTTGCCC CCCACCCCAT CCCGCACAGA ACCATCCCTG   60
CATTCCACAG GGGACTCGGG CAAGGGTGCC GAAGATAGAC AAGAGGCACA CAGAGACAGA  120
CCAACTGGCA GCCAGGCAGC CCCAGAGGAG AGAGACATTC AGACAGAGGA AAGTCTCCCT  180
GCCCCTCATT CCTTCCAAGA TGAGAAAAAC TTGCCGCCAC CCCCAGACAC TGATGCCAGG  240
GAGGTGGGAG GAAGAAGTGG GAAATTTCCC TTCCCAGTAC CCCCAGAAGAAC GTCTGAGCCT  300
TCAATGTTGA ATTTTTTCTT TATTAAAATT ACTTTTATCT TATAAAATCA ACTAATCAAA  360
AATGATATAG ACGACAGCAC TGGCTCTGTG AAGGTGGCAT CTTTCTGGGC AGGCAGGCCA  420
TGGGGCATGG AGGAGGGTGC AAAGATATGG GTTGCTGTCT TCTGGCCTCC AGCTGCATGG  480
AGGCCGGCCC AGGGTCTAGG GTGTGCACTG GGCAAGGGCA GGGCGGCAGG TGTCAGGCCG  540
GCTTGACAA TGAAACCCTG ACCTTGCTGC ATTCCTTTTG CTTCACCAC CACTAGCTTC  600
TTTGGAATCT TGGGGTGGGG GTCATCTTTG GGGATTATGG CTGCCACCCG GGATTTGAGT  660
GTAGGGAGTG TGGGAGCAGC CTTGGCAGAT GGGGCACCCG TGCCCTGCAG GTGTTGACAA  720
GATCCGCCAT CTGTAATGTC CTTGGCACAA TAAACCAAAA TGTCAGTTTC AAAAAA   777

```

(2) INFORMATION ON SEQ ID NO. 31:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 501 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

CCGGATTCCG CCCC GCCCGC TGC GATCCG TTCCGCTCCC CACAACCCGC TCTGTGGCGG   60
GGCTTCCGGT CGGGAGGGTC CGCCAGCTCT CGCGTCCTTT GCTGGGTCCA GACACCGGTT  120
CCGTTGCAAA CATTTTAAA GGGCTGGTTA TTCTTCCTGA AATGAGTTTG GTGATTAGAA  180
ATCTGCAGCG AGTCATCCCC ATCAGGAGAG CGCCACTTCG CAGTAAGATC GAGATTGTAA  240
GGAGGATTTT AGGAGTGCAG AAATTTGACC TGGGGATCAT CTGTGTTGAC AACAAGAATA  300
TTCAGCACAT TAATAGAATC TACAGAGATA GAAATGTCCC AACCGATGTG CTTTCTTTTC  360
CATTTTATGA GCATCTGAAA GCAGGTGAAT TTCCCCAGCC TGATTTTCCA GATGACTACA  420
ATTTGGGAGA CATTTTCTTA GGAGTGGAGT ATATCTTCCA TCAGTGTAGA GAAGATGAAG  480
ATTACAATGA CGTCCTGACT G

```

(2) INFORMATION ON SEQ ID NO. 32:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1104 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

ATTTTGACCC TAAACTTTTG GAAGGAAAAG TAAAGGAGGA TCCTGACCAG GGGGAATCCA 60
TGAAACCTTT AACCTTTGCA AGGTTCTACT TGCCAATTCT GGTTCCCAGC GCAAAGAAGG 120
CCATATACAT GGATGATGAT GTAATTGTGC AAGGTGATAT TCTTGCCCTT TACAATACAG 180
CACTGAAGCC AGGACATGCA GCTGCATTTT CAGAAGATTG TGATTCAGCC TCTACTAAAG 240
TTGTCATCCG TGGAGCAGGA AACCAGTACA ATTACATTGG CTATCTTGAC TATAAAAAGG 300
AAAGAATTCG TAAGCTTTCC ATGAAAGCCA GCACTTGCTC ATTTAATCCT GGAGTTTTTG 360
TTGCAAACCT GACGGAATGG AAACGACAGA ATATAACTAA CCAACTGGAA AAATGGATGA 420
AACTCAATGT AGAAGAGGGA CTGTATAGCA GAACCCTGGC TGGTAGCATC ACAACACCTC 480
CTCTGCTTAT CGTATTTTAT CAACAGCACT CTACCATCGA TCCTATGTGG AATGTCCGCC 540
AGCTTGGTTC CAGTGCTGGA AAACGATATT CACCTCAGTT TGTAAGGCT GCCAAGTTAC 600
TCCATTGGAA TGGACATTTG AAGCCATGGG GAAGGACTGC TTCATATACT GATGTTTGGG 660
AAAAATGGTA TATTCCAGAC CCAACAGGCA AATTCAACCT AATCCGAAGA TATACCGAGA 720
TCTCAAACAT AAAGTGAAAC AGAATTTGAA CTGTAAGCAA GCATTTCTCA GGAAGTCCTG 780

GAAGATAGCA TGCCTGGGAA GTAACAGTTG CTAGGCTTCA ATGCCTATCG GTAGCAAGCC 840
ATGGAAAAAG ATGTGTCAGC TAGGTAAAGA TGACAACTG CCCTGTCTGG CAGTCAGCTT 900
CCCAGACAGA CTATAGACTA TAAATATGTC TCCATCTGCC TTACCAAGTG TTTTCTTACT 960
ACAATGCTGA ATGACTGGAA AGAAGAACTG ATATGGCTAG TTCAGCTAGC TGGTACAGAT 1020
AATTCAAAAC TGCTGTTGGT TTTAATTTTG TAACCTGTGG CCTGATCTGT AAATAAAACT 1080
TACATTTTTC AAAAAAAAAA AAAA

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1104

(2) INFORMATION ON SEQ ID NO. 33:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 810 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GCCATCCTTT	ATCATCCACA	GCAATCCCAT	CTGGTTGGGA	GCACTGCTCT	GGGTCTCACA	60
CTGCCCCTCC	TCTATCCTAG	GGAGCCTGAG	GCCCAGGGGT	GGAAAGATCC	AGTTGCGGGT	120
GGGGGGTAGT	GAACCGTGCA	GGATAATGAA	AGCAACTTGC	TTTGGAAATG	ACCTACCGCT	180
ACCCGTTGTC	TGAGACTGAG	ATTATCTCAG	ACTGTCTTCT	GGCTTCTGCC	AAAACACTCC	240
CTTAACAGAA	AGCACCGAGG	GGATGGGGGT	AGGGGGGTTG	GGGAGAGTGA	GGCTTGAGTG	300
TGAAGGAAGT	CTCATATATG	CAGAGCTGAA	ATCTCCCTCT	TTGTATGTCC	ACACTTTTGT	360
CTTGTTCTCT	AGACTGATTC	TTGCTATTCC	AAATCCTCTT	CCACGTTGAC	AGCCCTTCAG	420
CATATTTCAAC	ACTCCTCTCA	GCATCCTCCA	CTTCCCCCAT	CTCTCCAAGC	TGAACCTGGT	480
TCACAGGGTG	GGATTGTGTA	TGTGCATGCA	GGAGGTGGGG	GTGGACAGTG	CCCTGGGCTG	540
GAATCCCCCT	TAGTTCTAAG	TGCCTCCTTG	CCC GCAGCTT	CGAGAGCTGT	GCCCAGGAGT	600
GAACAACCAG	CCCTACCTCT	GTGAGAGTGG	TCACTGCTGC	GGGGAGACTG	GCTGCTGCAC	660
CTACTACTAT	GAGCTCTGGT	GGTTCTGGCT	GCTCTGGACT	GTCCTCATCC	TCTTTAGCTG	720
CTGTTGCGCC	TTCCGCCACC	GACGAGCTAA	ACTCAGGCTG	CAACAACAGC	AGCGGCACGT	780
GGAAATCAAC	TTGTTGGCCT	ATCATGGGGC				810

(2) INFORMATION ON SEQ ID NO. 35:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 826 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TGGAAATCAT	GGCAACTACA	CAGGATGTTG	CTTACCAGGA	CGGAGTTTTG	GTATCTTAGT	60
ACTGAAGTTA	GCACTATGTT	TACATGCAAA	AGATTAAGGA	AAAAACCCTT	AAAGTGGACA	120
GGTATCCAAA	GTTCAATTTT	TGTGACTCAT	CAAAGTGACA	AAAGACTTGT	AACAACCTTG	180
CCTGGACTTT	TTTCATTTTA	CAACAGTTCA	TCCATTGACA	ATGATTTTGT	TCTCTGCTCC	240
ATATTTTTTA	ATCCCTTAAG	CATTTGATGA	AACACTCTTT	AGTGCTATAT	GCATTTTCTT	300
ACTTTTGTTA	AAAATGTGAC	AATTGTCAAA	AAATGCACTA	AAATGTAAAT	GGAGATTGAA	360
CAAGTTCAC	TTCCAGCTTA	TAGGCAACTT	TATACAGACT	TGAACATTTT	CTCCAGTTGT	420
TTAGTAAAAG	TGAAAGAGAA	AGGGTTTTTC	CTGCCACAGG	ATATAACTTT	TTTTTATATA	480
ACAAGCATAA	CACACCACTG	CTTTTGGTGG	AAAAGTGCAG	AATAGTATGT	ACCTTTTATG	540
AAGAAAAATG	TAATTTACAA	TATTCAGTGA	GAATGTTACT	GCTGATTTTC	TTTTCCAAGG	600
TGTAGAATAT	TCTTTGATTT	ATAGAATTCA	TTTTTGACCC	AGATGATGGT	TCCTTTACAG	660
AACAATAAAA	TGGCTGAACA	TTTTCACAAA	TAGAGTGTA	CGAAGTCTGG	ATTTCTGATA	720
CCTTGTCATT	TGGGGGATTT	TATTTTACTT	TGTTGCTTTA	AAATTCAATG	CAGAGAAGTT	780
GTTGACTGTA	GGGGAAATAA	AGTTAATTCA	AATTTTGAAA	AAAAAA		826

(2) INFORMATION ON SEQ ID NO. 36:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 578 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GTTCTTAACT	GTTCCATTTT	CCGTATCTGC	TTCGGGCTTC	CACCTCATTT	TTTTCGCTTT	60
GGCCATTCTG	TTTCAGCCAG	TCGCCAAGAA	TCATGAAAGT	CGCCAGTGGC	AGCACCGCCA	120
CCGCCGCCGC	GGGCCCCAGC	TGCGCGCTGA	AGGCCGGCAA	GACAGCGAGC	GGTGCGGGCG	180
AGGTGGTGCG	CTGTCTGTCT	GAGCAGAGCG	TGGCCATCTC	GCGCTGCGCC	GGGGGCGCCG	240
GGGCGCGCCT	GCCTGCCCTG	CTGGACGAGC	AGCAGGTAAA	CGTGCTGCTC	TACGACATGA	300
ACGGCTGTTA	CTCACGCCTC	AAGGAGCTGG	TGCCCACCCT	GCCCCAGAAC	CGCAAGGTGA	360
GCAAGGTGGA	GATTCTCCAG	CACGTCATCG	ACTACATCAG	GGACCTTCAG	TTGGAGCTGA	420
ACTCGGAATC	CGAAGTTGGA	ACCCCCGGGG	GCCGAGGGCT	GCCGGTCCGG	GCTCCGCTCA	480
GCACCCTCAA	CGGCGAGATC	AGCGCCCTGA	CGGCCGAGGC	GGCATGCGTT	CCTGCGGACG	540
ATCGCATCTT	GTGTCGCTGA	AGGCCTCCCC	CAGGGACC			578

(2) INFORMATION ON SEQ ID NO. 37:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 799 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AGCTTTTGGT	CACACTTTAA	ATAGCAGTCC	CAGAATGATT	TCACTACAGA	CTCTCTGGAA	60
AGCCTGGGAG	CTGAATTCCG	GAAGATCCCC	ACATCGATGA	AAGCAAAGCG	AAGCACCAAG	120
CCATCATCAT	GTCCACGTCG	CTACGAGTCA	GCCCATCCAT	CCATGGGTAC	CACTTCGACA	180
CAGCCTCTCG	TAAGAAAGCC	GTGGGCAACA	TCTTTGAAAA	CACAGACCAA	GAATCACTAG	240
AAAGGCTCTT	CAGAACTCT	GGAGACAAGA	AAGCAGAGGA	GAGAGCCAAG	ATCATTTTTG	300
CCATAGATCA	AGATGTGGAG	GAGAAAACGC	GTGCCCTGAT	GGCCTTGAAG	AAGAGGACAA	360
AAGACAAGCT	TTTCCAGTTT	CTGAAACTGC	GGAAATATTC	CATCAAAGTT	CACTGAAGAG	420
AAGAGGATGG	ATAAGGACGT	TATCCAAGAA	TGGACATTCA	AAGACCAAGT	GAGTTTGTGA	480
GATTCTAACA	GATGCAGCAT	TTTGCTGCTA	CCTTACAAGC	TTCTCTTCTG	TCAGGACTCC	540
AGAGGCTGGA	AAGGGACCGG	GACTGGAAAG	GGACCAAGAC	TGAACAGACT	GGTTACAAAG	600
ACTCCAAACA	ATTTTCATGCC	CTGTGCTGTT	ACAGAGGAGA	ACAAAATGCT	TTTCAGCAAGG	660
ATTTGAAAAC	TCTTCCGTCC	CTGCAGGAAA	GGATTGACGC	TGATAGAAGA	GCCTGGACAG	720
ATGTAATGAG	AACTAAAGAA	AACGATGGCT	GGAGATGACA	TTTATCCAGG	GTCACCTTGT	780
CAGGCCCTAG	GACTTAAAT					799

(2) INFORMATION ON SEQ ID NO. 39:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1743 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

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AATTTATTTT TTTTTCATGG TCTGTCAGGT TTTATTTATA GAGTCTGGTG AACTTGAACT 60
AGAGAAAGCT GCAAAAAGTG GTTTGGAGAG CATGGCAGGG CCATGGAGAA GGGCTAATAG 120
AAGCAGGTCC CTTGCCCAGA CCCTCAGGGA GCCCTTTTGG TGGATAGCGG ACACCTGAGG 180
CAGGAGGTGG CAGGGGCCAA GTCCAGGCAG GCAGCAGCAG GGCTGCAACT GAGAGCTGAG 240
GCTGGAGAGG TAGCGCTCGC CCTAACCTGA TCCTGCAGGT CTCAGGCCCT GGGGTCATAT 300
ACTCGCCCCA TGAAGACAGG GAACTTGTGC TGCTGGTCCC AGAGCACGAA GAGGAAGGGC 360
TGCTGCACTT CAAAGACCAG CAGGGTGCGG GCCACAGAGA TGGCGGAGGC TGCAGCCGCC 420
TCCACCCCAG TCTCTGTCAG TTCCAGCACT GTCTGGTGCT GCATCGCAGA AACCTGAAGA 480
TCTGGGTCCT CTGTCAGCCC ACACAGGTTA AGGTCATAAG AAAAAATCGAA GAATTCCAAT 540
TTCTCCATGA TTGAGAGCAT ATCCTGGCTG GTCGTCACTT TGATGCGGGG TAGTGTTAGG 600
AGAGTGGGCT GGAACCTGGA CATCTCCAGT TTCTCCATGA TGGCCTTGAA AACAGAAGGG 660
CTGAGAGCCT GTTCCATGTC TTCAAGACGA TGTTTCAGGT TCTGGGGTAC CAGGATCACC 720
AAACTCAGAT TGTGGGAGAG CTGCAGCTGC CCCACCTTGG CTTTCAAAGT TTGGTCAATG 780
AAATGGGCCA CAGGGTACTT CTTGCTATTC ATCATGGGCA CTTTTATAAC TGAGTTTTTG 840
AAGTGAAAGG GTTCCATTCT GGTTTCTTG GGATCAAATG TTGTCTTCCA CTTGGCACTC 900
AGGTAGATAG CATTGAGGAG GACAAGGCGG GTATCGGAGG GCAGACTGTC TAGCAGCCGG 960
CTGATCTTGT TGTTGGTGTT CTTGGCCACC CAGGTGTTGA TGAGCTCCAA AGTTGAATAG 1020
CAAGAAGTAC CCTGTGGCCC ATTTCAATTGA CCAAACCTTG AAAGCCAAGG TGGGGCAGCT 1080
GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC CAGAACCTGA AACATCGTCT 1140
TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG GCCATCATGG AGAAACTGGA 1200

GATGTCCAAG TTCCAGCCCC CTCTCCTAAC ACTACCCCGC ATCAAAGTGA CGACCAGCCA 1260
GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT TTTTCTTATG ACCTTAACCT 1320
GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG ATGCAGCACC AGACAGTGCT 1380
GGAAGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC GCCATCTCTG TGGCCCGCAC 1440
CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG CTCTGGGACC AGCAGCACAA 1500
GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCAGGGGCC TGAGACCTGC AGGATCAGGT 1560
TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTTCAGTTG CAGCCCTGCT GCTGCCTGCC 1620
TGGAATTGGC CCCTGCCACC TCCTGCCTCA GGTGTCCGCT ATCCACCAA AGGGCTCCCT 1680
GAGGGTCTGG GGCAAGGGAC CGTGCTTCTA ATTAAGCCCT TCTTCCAATG GGCCTTGCAT 1740
GGC

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1743

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GCCAATCGAA	TCGTCCTGGG	AGGCTTTTCA	CAGGGCGGGG	CCCTGTCCCT	CTACACGGCC	60
CTCACCTGCC	CCCACCCTCT	GGCTGGCATC	GTGGCGTTGA	GCTGCTGGCT	GCCTCTGCAC	120
CGGGCCTTCC	CCCAGGCAGC	TAATGGCAGT	GCCAAGGACC	TGGCCATACT	CCAGTGCCAT	180
GGGGAGCTGG	ACCCCATGGT	GCCCGTACGG	TTTGGGGCCC	TGACGGCTGA	GAAGCTCCGG	240
TCTGTTGTCA	CACCTGCCAG	GGTCCAGTTC	AAGACATACC	CGGGTGTCT	GCACAGCTCC	300
TGTCTCAGG	AGATGGCAGC	TGTGAAGGAA	TTTCTTGAGA	AGGTGCTGCC	TCCTGTCTAA	360
CTAGTCGCTG	GCCCCAGTGC	AGTACCCCAG	CTCATGGGGG	ACTCAGCAAG	CAAGCGTGGC	420
ACCATCTTGG	ATCTGAGCCG	GTCGAGCCCC	TGTCCCCACC	CTTCCTGACC	TGTCCTTTTC	480
CCACAGGCCT	CTGGGGGCAG	GTGGCAAGGC	CTGGCCGGGC	CTTCCTTCCT	GGCCTTAGCC	540
ACCTGGCTCT	GTCTGCAGCA	GGGGCAGGCT	GCTTTCTTAT	CCATTTCCCT	GGAGGCGGGC	600
CCCCCTGGCA	GCAGTATTGG	AGGGGCTACA	GGCAGCTGGA	GAGAGGGGCC	CAGCCGCTGA	660
CCCCTACCT	CAGGACCTCA	CTCACTAGCC	CCGCTTTGGG	CCCCCTCCTG	TGACCTCAGG	720
GTTTGCCCA	TGGGGCCCTC	CCAGGCCCT	GCCCCAACTG	ATTCTGCCCA	GATAATCGTG	780
TCTCCTGCCT	CCACTCAGCT	GCTTCTCAGT	CATGAATGTG	GCCATGGCCC	CGGGGTCCCC	840
TTGCTGCTGT	GGGCTCCCTG	TCCCTGGGCA	GGAGTGCTGG	TGAGGAGGTG	GATCCCTTTG	900
AGGGGGGCCT	TCCCTCAGCT	GTTTCCCCAC	ACTGGGGGGC	TGGGCCCTGC	TCCCCCTTA	960
CCCTCCTTCC	CTGCAGGCCT	GGAGCCTGTA	GGGCTGGACT	GAGGTTTCAGG	TCTCCCCCA	1020

GCTGTCTCAC CCCACTTTG TCCCCACTCT AGAGCAGGGA GGCAGTGGGG GAGGAGTTGT1080
GTCTCGTCTT CTGTCTCCAT GTGGTTTTTG GGTGTTTTTC TTGTTGTGTC CTGGATTCCG1140
ATAAAATTAA AGAAATTGCT TCCTCAAAAA AAAAAAAAAA AAA 1183

(2) INFORMATION ON SEQ ID NO. 42:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 768 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GTTTTTTTTT	TTACTGCAGA	AAATTGGTGG	TATTTTCACA	TTCATAGTGT	TTCTATCCAA	60
TTTCAGTACC	CACATTTAAT	GAGGAAAAAA	TGTTTTACCA	ATGAAGGAGG	AATTCTTAAA	120
TTAGCTGTAA	TGTTAGGTTG	GAGAAAATTT	GGTATTTAGG	GTATTTTCAA	GGTACCATCA	180
AATCAGATTT	CTGTTTTTTT	GTTAAAAAAA	ATTTTTTTAA	TCAGTATTGT	TTTTACAAGT	240
AATATACTTT	GAAACTCTTG	AACTAATAGT	CTCAAAAAC	CTAGAGGACA	GTCTGAGAAC	300
ACGTATTTCT	ATTGTTCTAA	ATAAATACAT	GTTTTTGAAT	AGTTCAATCA	TGAATTATTG	360
ACTATGTCTT	CATCAAAAGT	GTTAATCCCT	CTCAGGGTCT	CTGGTGAAGA	CCTTCAAGAG	420
TTTGGTTTTT	TCTCCCAGGA	AATTGGAAGG	TAGAATTGTA	AATTCATAGA	ACTTCTTTTA	480
TAATGGTGTA	CCTCAGCAGC	TGCCTTTCAA	TTTATGCCAA	GTCCTTACAG	AGTTTATACT	540
TGAATAGTAA	ATATGTCTTC	TGAGTTTTAC	AGTGTCTTAA	ACTCAATGCA	CATTTTTTTT	600
TCTTCTTTTT	CCACCCCTTC	TTGTTTGTAG	TTCATTATAC	CTGTCCTATT	ACAGAAGTGA	660
TTTCCTTCCT	GGCTGTACAT	GTTGGGGTGC	TGGATTTTTT	TCCGTGTCTT	TAGTCTTCGG	720
ATACATGTTC	TCTTCTTTAG	CTTGTGGTGA	ATACAGTAAT	TTGCATTG		768

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

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CCCTGCTGTG AAGTCCTGGC AGGTGTTGGT AATGTGTGGA AATGCAGTCA GCAAGTTTGC 60
TGGGGAGTTT GATAAAAGTA TAAAACAAAA CAAAAAAGC CTCGGTATAA TTTTGTTCCT 120
CGACTTCTTC TGTAGCTTTA CACCAGAAGG AAGGAATGGG CTACAGCAGG TAGTGGAGGA 180
AGAGGGGGGT GAGCAGGTGT ATTAAATAG CTTACGGGTA AGGCCTAAAA GGTCACCCCT 240
CGGCCCCCTC TCCAAAAGAA GGGCATGGGC ACCCCAGGA GAGGATGGCC CCAAAAACCT 300
TATTTTATA CATGAGAGTA AATAAACATA TTTTTTTAC AAAAATAACT TCTGAATTTA 360
TCAGTGTTTT GCGGTTAAAA ATATTCCTCT ATAGTAAATT ATTTATTGGA AGATGACTTT 420
TTTAAAGCTG CCGTTTGCCT TGGCTTGGTT TCATACACTG ATTTATTTTT CTATGCCAGG 480
CAGTAGAGTC TCTCTGCCTC TGAGGAGCAG GCTACCCGCA TCCCACTCAG CCCCTCCCTA 540
CCCCCAAGA TTTGATGAAA ATTCCAACCA TGAGGATGGG TGCATCGGGG AAGGGTGAGA 600
AGGAGAGCCT GCCTGCTCAG GGATCCAGGC TCGTAGAGTC ACTCCCTGCC CGTCTCCCAG 660
AGATGCTTCA CCAGCACCTG CCTCTGAGAC CTCGCTCTCT GTTCCAGCAA CCCTGGTTGG 720
GGGGTCAGAC TTGATACACT TTCAGGTTGG GAGTGGACCC ACCCCAGGGC CTGCTGAGGA 780
CAGAGCAGCC AGGCCGTCCT GGCTCACTTT GCAGTTGGCA CTGGGTTGGG GAGGAAGAGA 840
GCTGATGAGT GTGGCTTCCC TGAGCTGGGG TTTCCCTGCT TGTCCAGTTG TGAGCTGTCC 900
TCGGTGTTAC CGAGGCTGTG CCTAGAGAGT GGAGATTTTT GATGAAAGGT GTGCTCGCTC 960
TCTGCGTTCT ATCTTCTCTC TCCTCCTTGT TCCTGCAAAC CACAAGATAA AGGTAGTGGT 1020
GTGTCTCGA

```

(2) INFORMATION ON SEQ ID NO. 44:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 736 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

ATTCCTGGGT TGAAATATTT TGTAGGGATT GCTTATTATA TTATTTTAGC TGATGAACCT 60
CAGGACAACG GCTACAGACA CACACATACA TACACGCACA CAAAATCTCA GCTGTTGAAG 120
AGTGGGCTTG GAATCAGACT TCTGTGTCCA GTAAAAAACT CCTGCACTGA AGTCATTGTG 180
ACTTGAGTAG TTACAGACTG ATTCCAGTGA ACTTGATCTA ATTTCTTTTG ATCTAATGAA 240
TGTGTCTGCT TACCTTGTTT CCTTTTAATT GATAAGCTCC AAGTAGTTGC TAATTTTTTG 300
ACAACTTTAA ATGAGTTTCA TTCACTTCTT TTAAGTAT AGTACCAATA 360
ATTCATTAA CCTGTTCTCA AGTGGTTAG CTACCATTCT GCCATTTTTA ATTTTATTT 420
AATTTTATTT GCTTGAGCAC ACTGATCAAC CACTGAACCTG CCTTCTTCCA TTGTCCTGCA 480
ATGATATAAG GGTTACATTT TTGTGTATAT GGCTTTCATA GTTGGGATTT CAGAGCACTG 540
ATACCAGATA TTTTCAGTTT GTTCTCTGGG GGAATTTTCAT TTGCATCTAT GTTTTCTAGT 600
ATCTGTGATA ACTTGTTAAA TATTAATAAG ATATTTTGCT TCTATTGGAA CATTTGTATA 660
CTCGCAACTA TATTTCTGTA AACAGCTGCA GTCAAAAATA AAACACTGAA AGTTTTCATT 720
TTGCAGTGGA AAAAAA 736

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(2) INFORMATION ON SEQ ID NO. 46:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1159 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GGACCGTGTG TCGGCCGTGG CGCTGCCCAA GCTGCCCATC TCGCTCACCA ACACCGACCT 60
 CAAGGTGGCC AGCGACACAC AGTTCTACCC TGGCCTCGGG CTGGCCCTGG CCTTCCACGA 120
 CGGCAGCGTC CACATCGTGC ACCGGCTCTC ACTGCAGACC ATGGCCGTCT TCTACAGCTC 180
 CGCGGCCCCG AGGCCTGTGG ATGAGCCGGC CATGAAGCGC CCGCGCACCG CGGGCCCCGC 240

CGTCCACTTA AAGGCTATGC AGCTATCGTG GACGTCACCTG GCCCTGGTGG GGATTGACAG 300
 CCACGGGAAG CTGAGCGTGC TCCGCCTCTC ACCTTCCATG GGCCACCCGC TGGAGGTGGG 360
 GCTGGCGCTG CGGCACCTGC TCTTCTGCTT GGAGTACTGC ATGGTGACCG GCTACGACTG 420
 GTGGGACATC CTGCTGCACG TGCAGCCCAAG TATGGTACAG AGCCTGGTGG AGAAGCTGCA 480
 CGAGGAGTAC ACGCGCCAGA CCGCTGCCCT GCAGCAGGTC CTCTCCACCC GGATCCTGGC 540
 CATGAAGGCC TCGCTCTGCA AGCTGTGCGC CTGCACGGTG ACCCGCGTGT GCGACTACCA 600
 CACCAAGCTC TTCCTCATCG CCATCAGCTC CACCCTGAAG TCGCTGCTGC GCCCCCACTT 660
 TCTCAACACG CCTGACAAGA GCCCCGGCGA CCGGCTGACC GAGATCTGCA CCAAGATCAC 720
 CGACGTCGAC ATTGACAAGG TCATGATCAA CCTCAAGACG GAGGAATTTG TGCTGGACAT 780
 GAACACACTG CAGGGCGCTG CAGCAGCTCT TGCAGTGGGT GGGCGACTTC GTGCTGTACC 840
 TGCTGGCCAG CCTACCCAAC CAGGGTTCCC TGCTGAGGCC GGGCCACAGC TTTCTGCGGG 900
 ACGGCACCTC GCTGGGCATG CTTGCGGAAT TGATGGTGGT CATCCGCATC TGGGGCCTTC 960
 GAAGCCCAG CTGCCTGCCC GTGTATACGG CCACCTCGGA TACCCAGGAC AGCATGTCCC1020
 TGCTCTTCCG CCTGCTCACC AAGCTCTGGA TCTGCTGTCG CGATGAGGGC CCAGCGAGCG1080
 AGCCGGACGA GGCCTGGTG GATGAATGCT GCCTGCTGCC CAGCCAGCTG CTTATCCCCA1140
 GCCTGGACTG GCTGCCAGC 1159

(2) INFORMATION ON SEQ ID NO. 47:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 690 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

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AGAGCGGCCG CCCCTCTTTT TTTCTCTTTC TTTTTTTTTT TTTTTCGATA TCAGAAATGC    60
ATTTTAATTT TTATTTGAAA ACAACTTAAA TTTTtagACA AATGATTTTA GTATATAAAT   120
TTGCTTTTGT TTTTATACAG AATATAAAGA TTTCCCTCAT TAATCTTCCA TGTGAAGGGT   180
ATTACAAGCC TGGAGGAAGA TACTTTCTGC ACACAAGTAT GTATCTTATG TGTGCAGTAT   240
TGGAAACCAA TGGTGTAGTG CTCCTACACA TAAATGGGGT CAAGTGACAT CACAAATTAA   300
AAGGGGGAAA GAGAAATATT CTAGTTAATC AGATGCAAGA AGCAAACAAG ACGCAAAAAC   360
TGTGCAAATA AGACCAAGCC AGTAACTTTA GTTACGACAC TGCAGATTAC ACTGGAATAA   420
CAGGTTTGTG AGGCTATAGT GTGCACCACA TTAAAACAGC AAGAAAGAGC TATTTATATA   480
GAAAGGCTGG AATGAGGGAT TTTTACTAAA GCAAATTAAC TTCTTGTCOA CTGCCAAAAC   540
AAAACAAAAC TGAGCATATG AGTGTTAGTA TACTGAAGGC ATGTTATACC AGTTTCTGTG   600
CAGCATGCTA AAAGTTAGAA CTTCTTCACT GGTGCTTATC AATCATTAAT AGTCACGTTT   660
TTGCCCTTC TTGCCAAATT TCGAGGCATG

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690

(2) INFORMATION ON SEQ ID NO. 51:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1186 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

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ACCATAGATT TATTTTAAAA GGGAAAATCT CACACATAAT TAAGCAGTGG AAAATGTGCT 60
CAATGCTATG GTGCGTCAGG CCCTCTGTCT ACCAGGTTTC TCCCGCTTTC TGCAGAGCTG 120
TGGACCCTGT ACGTACCAAA CAGGTGAACT TGGTCCATCT TTCCTTCTTC CTTTTTTTGC 180
ACATTTGTCAT TTATATCTTC CTGTACTAAA AGAAACAAAT TATTTATAAT TGGGGTGACA 240
ATATAAAGGA ACAAAGATG GGGCAATAGT TGCTTCCTAG CTGGAGCTGT AAGTCCATGT 300
TACAGAACT CACTATTTAA AAAGTTTAA AAGATTTATG AACCTTGTC TACAATTCGC 360
TGAATACTTA TTTGTCTTTT AAAGTCCCCT CGGTGTATGG ATCATCTTCG TCAGAATGCC 420
GTTGTTTCAT TGTGAATCAG GGGAAAATGT TAATCATTTG GAGACTGTTT TCTTATTACC 480
AAATGTACAA TCCATAAGAC AACTGAAAGC AACAACCTGCT GGGTTCCTG ACAAAGATTA 540
TAAAAATCAT CACGTTCAAA GTAGAGTTT TAGCCAAGGT CAAGAACTAA CCTGGGGCTG 600
AGTCAGCGTC TCTACCCACT TAAATAACAG CGTAAAGATC TTCACTAAA TTCGTTATGT 660
GGTCTGTCTG GATGTAAACC TATATATTTT CTTTTGAAAC AGAATCATAT CCTGCAGACT 720
CTTGGCACTC CTGCATAGCT TTGACCGAAT GTTCACTCTC ATCGTAATGG AAGATTTCTA 780
TCTATGCAGA TAATACATGT TTTTAAATAC TGTTTTCTGT TTAGTCCTCA ATCTTCCTAA 840
CTCAAATTGG GGAAGTGAAG GAGAGAAAGG TGTTTACCCC TGTTACCGTG CCATATTCTT 900
CTTGCTGCTT TTCAACCCCA CGTGATTGTT GATTGACGGT TCTGCTATAA TGTGCGTGCC 960
CTTCAAGTTT CAGAAAACCT TCCCAATCAT TTCACTTCAA TCTTAATTGA ACCCAAGAGT 1020
CAAAGTTATT ATTTTCTCCG AACGTGTTTG TGATCTTCTG TTATATTTTG GGGCATGTTA 1080
CCTTTATGGT ATATAAGCTG TAGTGCATAC TCTTTGTATT GCAAAAAACT GGTCAGTAAT 1140
TTATGTACAT GTATTCCACA TTTTAGTGTG CTGGAAGTGA CAATCC 1186

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(2) INFORMATION ON SEQ ID NO. 52:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

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GGGAGAAGGA GGAGGCCGGG GGAAGGAGGA GACAGGAGGA GGAGGGACCA CGGGGTGGAG 60
GGGAGATAGA CCCAGCCCAG AGCTCTGAGT GGTTTCCTGT TGCCTGTCTC TAAACCCCTC 120
CACATTCCCG CGGTCCTTCA GACTGCCCCG AGAGCGCGCT CTGCCTGCCG CCTGCCTGCC 180
TGCCACTGAG GGTTCCCAGC ACCATGAGGG CCTGGATCTT CTTTCTCCTT TGCCTGGCCG 240
GGAGGGCCTT GGCAGCCCCT CAGCAAGAAG CCCTGCCTGA TGAGACAGAG GTGGTGGAAG 300
AAACTGTGGC AGAGGTGACT GAGGTATCTG TGGGAGCTAA TCCTGTCCAG GTGGAAGTAG 360
GAGAATTTGA TGATGGTGCA GAGGAAACCG AAGAGGAGGT GGTGGCGGAA AATCCCTGCC 420
AGAACCACCA CTGCAAACAC GGCAAGGTGT GCGAGCTGGA TGAGAACAAC ACCCCCATGT 480
GCGTGTGCCA GGACCCACAC AGCTGCCCAG CCCCATTGG CGAGTTTGAG AAGGTGTGCA 540
GCAATGACAA CAAGACCTTC GACTCTTCCT GCCACTTCTT TGCCACAAAG TGCACCCTGG 600
AGGGCACCAA GAAGGGCCAC AAGCTCCACC TGGACTACAT CGGGCCTTGC AAATACATCC 660
CCCCTTGCCT GGACTCTGAG CTGACCGAAT TCCCCCTGCG CATGCGGGAC TGGCTCAAGA 720
ACGTCTTGGT CACCCTGTAT GAGAGGGATG AGGACAACAA CCTTCTGACT GAGNAAGCAG 780
AAGCTGCGGG TGAAGAAGAT CCATGAGAAT GAGAAGCGCC TGGAGGCAGG AGACCACCCC 840
GTGGAGCTGC TGGCCCGGGA CTTGAGAAG AACTATAACA TGTACATCTT CCCTGTACAC 900
TGGCAGTTCG GCCAGCTGGA CCAGCACCCC ATTGACGGGT ACCTCTCCA CACCGAGCTG 960
GCTCCACTGC GTGCTCCCTT CATCCCCATG GAGCATTGCA CCACCCGGTT TTTGAGACC1020
GTGACCTGG 1029

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(2) INFORMATION ON SEQ ID NO. 53:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 985 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ATCACTCTTT	CTCAGCTCGA	CTGGAGTTTC	TGCACCTTTG	CAGGGGCAAA	GTAAGTCCCT	60
GCACCCTGAA	CCACCCCCCA	TTCCTGTTCA	TTTCAGCAGA	TAATGATGGA	GGGGGGGGGG	120
TGTCCATCGT	GCTGAGGGTG	TGACCGCAAG	AGGGTGAAAA	CTTCCAGCCA	ACTTTCTCAG	180
TCCTTTCTCT	TGCGAGAGGG	AAGCCACCTG	CTATACAAAC	TAATACCCCC	TGCCTTGACC	240
CCTTCCCCAC	GACTCAGTTG	ACAGAAGGAT	ATACTTTGTT	ATAACTTATT	ATTTTGTTCT	300
CTGTAAATAC	AAGATGTTTA	TAGGAAATAT	GTATTCTGAA	CTCTATCTGC	AGAATGAGTC	360
ACTACACCAA	AATAGTTCTA	TTATTTAGAA	TGTGTTAATT	TTAAAGGGAC	CTGATAGGTA	420
TTTATTTACA	TATGCGATCC	ACATTTGTGT	GAAAGCATGT	GATCATACTA	ACCCAGCCTC	480
CTGGAATGTC	GCTGTACGAT	GATTGATGTC	TTTTTCTCAG	TCCATAGTTA	CAATTGTTTA	540
GTATGCTAAT	CAGTCCAGTT	CCCTGAGGTT	TAAGATCAAA	TATAAATTAC	TCTGCTTTTC	600
GACTCATTCA	GGTAGCATTG	TACCTGAACC	TGATTGCTAC	TTTTTTCATCT	TAAATATTAT	660
ATTTCCTCAT	CTAATCTGCC	TTCCCCTCAT	CCACAGACAT	TTGGAGAAGG	AAATGGGAGG	720
GTGTCTGTTA	TCCCTTTCTC	TTTGCTTTGT	CCCCGTTGTT	AGACTGGCAG	CGTCAGTTGC	780
TCGGTGGGCT	TGGTTAGAGC	CGTGGGTGAG	GCAGGTGGCT	GGCGGGGACA	GGGAGAGGCT	840
GAGAGGGAAG	TGGTGGCATT	TACTGCTCTG	ACACTTCCAC	TGTCCCTGCT	GGGGATGCTG	900
GGGCCAAGGC	CTGTGGGGCC	TGTGAAGTGC	ACAGCCAGGA	GCAAGGAACC	CACTAAATAC	960
TCCGTCAC TG	CATGTCCCCT	CTACA				985

(2) INFORMATION ON SEQ ID NO. 54:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 622 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

ATGTTTTTCA	TTTTTTTCAT	GTTATCTATC	CAAGCACTGT	TCCATGGTCA	GCAAGTCATA	60
TTTCATAATG	TGGATTTTCC	AAAATAATTA	TTGAATACAG	CTATTCTATG	GCTACTTTTA	120
GTGTTTTTGT	GGTATGTGGT	GTGGGAGTGT	TTATGGAATT	ACCAGTATCT	TAAATTTTCA	180
AAGGAACCTT	GGAAGTCTAT	CACTCTAAAT	GAAAGTCTGT	CACTCTACAT	GAATTATGTG	240
CTCAAATTTG	ACCAACTCAG	TTTAAGACAC	AAAACAGTAA	TTTGAAGAAG	GAAAAATGAA	300
GAGAGTTTCT	AGTTTAATGG	GTTAAATTTT	TGTTGTTGCA	ATAGTAAGTT	TAGTCTTCTT	360
ATAATATTTT	TAAATGAAAA	ATCATAGGTA	TTTGTTACCA	TGTGTGAAGA	TTACTTTGTT	420
AAAAGCAAAA	GTGTCGTGT	GATATGCTAA	ATGTTAATTA	CTGATTTTAT	ATGTTTAAAT	480
CACGCCAAAC	AAATTATGTC	TGTGCCATCC	AGGGTCTGTT	GTTAATCTTT	TTCTGAGTAC	540
TTGGATTGGG	ATAAAGGGCT	TGTACTATGC	ACTTTTTTATT	AATGAATAAA	TAGAAAACGT	600
TAGTAACAAA	AAAAAAAAAA	AN				622

(2) INFORMATION ON SEQ ID NO. 55:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1129 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

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GATTTTTATC TAGAAACTAT ATTTACTTAA ACCCCCCTCA GGAAAGAGGT TTTAAAATCA 60
AAGATGGGAA AATCGGAGAA AATTGCCCTT CCCCATGGCC AGCTTGTTCA TGGTATACAC 120
TTGTATGAGC AACCAGAGAT AAACAGACAG AAAAGCAAAT ATAAGTTGCC ACTAACCAAG 180
ATCACCTCTG CAAAAAGAAA TGAAAACAAC TTTTGGCAGG ATTCTGTTTC ATCTGACAGA 240
ATTCAGAAGC AGGAAAAAAA GCCTTTTAAA AATACCGAGA ACATTAAAAA TTCGCATTTG 300
AAGAAATCAG CATTCTAAC TGAAGTGAGC CAAAAGGAAA ATTATGCTGG GGCAAAGTTT 360
AGTGATCCAC CTTCTCCTAG TGTTCCTCCA AAGCCTCCTA GTCCTGGAT GGGAGCACT 420
GTTGAAAATT CCAACCAAAA CAGGGAGCTG ATGGCAGTAC ACTTAAAAAC GCTCCTCAA 480
GTTCAAATTT AGATTTCAGA TTTTCAGTATG TGTGTAAAC ATAATTTTTC CCATATCCCT 540
GGACTCTTGA GAAAATTGGT ACAGAAATGG AAATTTGCCT TGTGCAACA TACAATTGCA 600
AAAGATGAGT TAAAAAATT ACATACAAAC AGCTTGATT ATATTTTATA TTTTGTAAT 660

ACTGTATACC ATGTATTATG TGTATATTGT TCATACTTGA GAGGTATATT ATAGTTTTGT 720
TATGAAAGTA TGTATTTTGC CCTGCCCCA TTGCAGGTGT TTTGTATATA TACAATGGAT 780
AAATTTTAAG TGTGTGCTAA GGCACATGGA AGACCGATTT TATTTGCACA AGGTACTGAG 840
ATTTTTTTCA AGAAACAGCT GTCAAATCTC AAGGTGAAGA TCTAAATGTG AACAGTTTAC 900
TAATGCACTA CTGAAGTTTA AATCTGTGGC ACAATCAATG TAAGCATGGG GTTTGTTTCT 960
CTAAATTGAT TTGTAATCTG AAATTACTGA ACAACTCCTA TTCCCATTTT TGCTAAACTC 1020
TAATTTCTGGT TTTGGTATAT ATCCATTCCA GCTTAATGCC TCTAATTTTA ATGCCAACAA 1080
TAATTGGTTGT AATCAAATTT TAAATAATA ATAATTGGGG CCCCCCTT 1129

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(2) INFORMATION ON SEQ ID NO. 58:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 877 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CACACTGAGG	GTTTTTAACA	CCATTCTCCC	CCACTTCTCT	CCTGGGTGAC	ATAAGAGAGA	60
AATAACCTGT	AGTACAGCAG	CTAAAGTATT	CTCCTTTTCAG	AGAATTTTTT	TGGAGGTCTC	120
TAATATATAT	TTCCCCCTTG	TCTCTGTGAT	CTCTTATTTA	TACTATATTA	TTGTCCCATG	180
TACTTTCTAA	ACTGAGCTTG	GAACATTTAG	TATTCCTGCA	ATTGGACTTC	CCACTTAACA	240
ATTATACAGA	CTTTGCTTTT	AGAAATAGAT	TAGGTTCCAA	ACAGAAAGTT	CAAGTGTAAC	300
AACAACAATA	AAAATAGATT	ATGAAACAGG	CTATAATTGG	CTCTTTTGGA	TTTGATAGGG	360
GCAAGATGAA	AGGCAACTTT	CTTGCTTTTG	AAATCATGTT	GGGTAAGAGG	TAAGGAATCC	420
AGCTACAATT	TTATTAGTGC	TTGAAACGGG	CTTCCTTGAA	TTCTCCAGGC	CCTATCATTT	480
TTTTTTTTCT	TACTAATCAG	AAGAGAGCTG	GGGTAGAAGC	CCCATGTTTG	TATTCATGA	540
AACACGTCGG	GTTGGAGTAA	AGGCAAAAAC	AGCTAGACAC	ACCAGGTGTG	TCTGTTTGAC	600
ATTTATAAGC	TGGCACTCAT	CAACACTCCT	GTTTCTCCTT	TCTCTGGGAC	GTGTGGATTA	660
AGGGGTGTGA	GTTGTGGGAA	GAATTGCCCT	CGTACCTCCT	GGATTATTA	TTTTTCTCAA	720
ATACCAACCA	GTAAGATCCC	AAATAACTTG	AGAAAAATTG	TTTCCTGATC	TGTCCACTTC	780
TGGTGTCAAA	GATTTTACTC	ATCTTCTTAG	TACATTCTAT	GTATTTTATA	TGTATAATTT	840
TATACAATTA	AAAATAGATT	TTTGTCTAGT	GAAAAAA			877

(2) INFORMATION ON SEQ ID NO. 59:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1329 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

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GTCGGGGAGC GCGGGGCCGG GGGCCAGGGG ACCCGGGGCC ACGGAGAGCG GGAAGAGGAT 60
GGATTGCCCG GCCCTCCCCC CCGGATGGAA GAAGGAGGAA GTGATCCGAA AATCTGGGCT 120
AAGTGCTGGC AAGAGCGATG TCTACTACTT CAGTCCAAGT GGTAAGAAGT TCAGAAGCAA 180
GCCTCAGTTG GCAAGGTACC TGGGAAATAC TGTTGATCTC AGCAGTTTTG ACTTCAGAAC 240
TGGAAAGATG ATGCCTAGTA AATTACAGAA GAACAAACAG AGACTGCGAA ACGATCCTCT 300
CAATCAAAAT AAGGGTAAAC CAGACTTGAA TACAACATTG CCAATTAGAC AAACAGCATC 360
AATTTTCAAA CAACCGGTAA CCAAAGTCAC AAATCATCCT AGTAATAAAG TGAAATCAGA 420
CCCACAACGA ATGAATGAAC AGCCACGTCA GCTTTTCTGG GAGAAGAGGC TACAAGGACT 480
TAGTGTCATCA GATGTAACAG AACAAATTAT AAAAACCATG GAACTACCCA AAGGTCTTCA 540
AGGAGTTGGT CCAGGTAGCA ATGATGAGAC CCTTTTATCT GCTGTTGCCA GTGCTTTGCA 600
CACAAGCTCT GCGCCAATCA CAGGGCAAGT CTCCGCTGCT GTGGAAAAGA ACCCTGCTGT 660
TTGGCTTAAC ACATCTCAAC CCCTCTGCAA AGCTTTTATT GTCACAGATG AAGACATCAG 720
GAAACAGGAA GAGCGAGTAC AGCAAGTACG CAAGAAATTG GAAGAAGCAC TGATGGCAGA 780
CATCTTGTCG CGAGCTGCTG ATACAGAAGA GATGGATATT GAAATGGACA GTGGAGATGA 840
AGCCTAAGAA TATGATCAGG TAACTTTCGA CCGACTTTCC CCAAGAGAAA ATTCCTAGAA 900
ATTGAACAAA AATGTTTCCA CTGGCTTTTG CCTGTAAGAA AAAAAATGTA CCGGAGCACA 960
TAGAGCTTTT TAATAGCACT AACCAATGCC TTTTATAGAT TATTTTGTAT GTATATATCT 1020
ATTATTCAAA AAATCATGTT TATTTTGAGT CCTAGGACTT AAAATTAGTC TTTTGTAAAT 1080
TCAAGCAGGA CCCTAAGATG AAGCTGAGCT TTTGATGCCA GGTGCAATCT ACTGGAAATG 1140
TAGCACTTAC GTAAACATT TGTTTCCCCC ACAGTTTAA TAAGAACAGA TCAGGAATTC 1200
TAAATAAATT TCCCAGTTAA AGATTATTGT GACTTCACTG TATATAAACA TATTTTATA 1260
CTTTATTGAA AGGGGACACC TGTACATTCT TCCATCATCA CTGTAAAGAC AAATAAATGA 1320
TTATATTCA

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(2) INFORMATION ON SEQ ID NO. 60:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 697 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

GTAGGCGCTA	GTCTGGGCGC	AGAGGTTTCT	GGGAGCCAAG	AGTGGAATAT	GCGTCTGTAT	60
GATCTTTCGA	GCCTGCTGCA	TCGGACCTCG	GCCAGTCATA	AAAGATGACA	ACAGCAGCCA	120
GGCCAACCTT	TGAACCTGCC	AGAGGTGGAA	GGGAAAAGG	AGAAGGTGAT	TTGAGCCAAC	180
TTTCAAAGCA	GTATTCAAGC	AGAGACCTAC	CCTCTCATA	AAAGATAAAA	TACAGACAGA	240
CTACTCAGGA	TGCCCCTGAA	GAGGTTCTGT	ACCGTGACTT	CAGGAGAGAG	TTGGAAGAAA	300
GAGAGAGAGC	TGCTGCAAGA	GAGAAAAATA	GGGATCGTCC	AACCCGAGAA	CATACAACCT	360
CCTCTTTCAGT	GTCAAAAAAG	CCACGGTTAG	ACCAGATTCC	TGCCGCCAAC	CTTGATGCAG	420
ATGACCCTCT	AACAGATGAG	GAAGATGAAG	ATTTTGAAGA	AGAAAGTGAT	GATGATGATA	480
CTGCAGCTCT	TCTTGCAGAA	CTGGAAAAAA	TAAAAAAGA	AAGAGCTGAA	AAGGGCCAAG	540
GGCCAGGGAA	GCGACCAAGG	GCCAAAAAAG	CTTTAAGGGG	GGGAAGGGTT	TCGTTTTGGG	600
AAAACATTGG	TTGGGCGGGA	AACCTTTTCC	CTTTAATCTT	GAGCTTGGCC	CATTCCAAGC	660
TTAAGGCCGA	CTTTGAAAAG	TTTGAAAGGA	GGGTGGG			697

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1389 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

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CGAAGAATAG AATTGGCCAG GACCTAGGTT CTCATATTCT TGGTATTCCT CCTGGATGGA 60
AAGGCTGTTG GCATCAATAG GGGACAGAGG CTGATGCTGG AGTGGCCAGT AGAGGTGGTG 120
GAGCAGAGCA GCCATCTTTT AAGTGGGGCT GTATCAGGCT GGGTTTATTT AAAAGCAACA 180
AAATGTTTTG GTTAAGAAAA TTATTTTGCT TTCAGTGTA ATCTTCGCAG TGTTCTAAAC 240
AAAGTTCAGT CTTCTGCTCG CCCCTTTCCC TCACTGATGT CTGCACTTGG TTGAGGTCTC 300
CTGGAGCCTC ACAGGCTCTG CTGTTCTCCA CTTCTCACCT GCCATCCACG CCCTGCAAGC 360
TCATGCAAAC ACCCTTTCTT CCTCCTGCGG CAGAGTTGTT CAGGTTGCCT GGGCAGGGGC 420
TTAAACAGTG CCAGCCCCTG CCATCCCCAA GCTATTGTTA AGCCCCCAG GCGTCCTCCA 480
CCCACGCCCC CTAGCCTGCC ATGTCCACAG TTCCTTGGGC TGCTGAGGGG CTAGTGCAGT 540
GGTCCTGACC TCTCTTATCA AGAGCACACT TCTTTGCTGG TTGCTCCTTT TGAGCATATG 600
CGTGTGATTA TTTGGAACAG TTAGACTTGC CACGTTGGGT CAGTTTTAGA AATTGTTTCT 660
AGCTAGAGGG ACTGGTGTCC TTCCAAGTCT AGCATTGGG GTATGGAAAA TTGTTGTGGT 720
GTGTGGTAGG GTTTTTGTTT TCTTTTTTGA GTTTTTTTTC CCCCTTTAGT CTCCTGGCTT 780
TTTCCTTTCC CTTCCCTTCT CCACTGGCCN AGCTTGGGCC TCATCCTCAT GTCATCCTTC 840
TAGGAAGGCG CCTGCCCAT CTTGTCTGCC GGCAGCATGC ATCCAAGGCC AGAGCTCCTC 900
CCTGCAGACT GGGCTGGTGC CTCCTCCGCT TCAGGGTATG GGAGTTGGTG AAGGGGCTTT 960
CAAAAAATAA TAAGAAAAAA AAGGTAAAGT CTTTGGTAGC TTCTATCCAC TCAGATCCTG1020
GAAGGCAGCA AGGTTTTGTG GATCTAGATT CATTAGGAAT GTCTTCTTGT CAGCCAGGCC1080
AGGACCCGGG CTTGCCAAGA GCAGAGGCC TCCAGCAAC CAGGATACCA CCACTTTGGG1140
GGCTTTGTGT ACAGAGGTCC GGGTCTGAGA CCTCATAGGC TGCAGAAATC TGGGGCAGCC1200
ACCATCAAGA AGCCCCTCTC AGGGGCCAGA ACTCCTTTGC CAGCGTGGAT TTCTCAAGTC1260
GGGACTGCAT AATTAAAGCA GTTGCAGTTT TATTTTTTTT ACAGCTTTTT TCCCAAAAAT1320
GATTTGTAGT TGTGTGTGCA GCACTTCGCC CTGATATGTG TGCTCTACAA TAAAAACCAA1380
ATCTAATAT

```

(2) INFORMATION ON SEQ ID NO. 62:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 535 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TGTATTGAGG	TAATAAATTG	TTTTACTGAC	AATTTTTCCT	TTTTCTACAC	TAAAACAATA	60
TGTGATATAT	TTCCCCCTCT	GAAGAGGCAA	TTCATTAAAC	TCTCAAATTT	TCTATAGAAT	120
CAAGATAGAA	CCTTTAGATA	CTCCAACCTCA	CCAAAATGTA	AAAAAACTAA	CAAAAATATT	180
TGGTCTTCAA	TAATGCTAAA	TATCTACATT	TTTAGAATTT	ATCAACATTT	AACTAGATAA	240
TTGGGCATGT	CTTAATTATG	CATGTACTTA	TCCATACTAA	TAAAATTGAC	AATGCTAGTG	300
CATACTTATT	GGTTTAGTCC	TATTATCAGG	ATATAATCAT	CTGTGAGGAG	GATATTTTAA	360
ATACTGTAAA	TGATAACAGT	TAATGATATA	CACATTTAGA	CTGAGTTGCA	CACTGGCAGG	420
GAGACCAAAA	ACATTACTTC	CATACTTGTC	TCATGATTCT	TTTTTTTTTG	AGAGAGTCTC	480
ACTCTGTCGC	CAGGCTGGGA	GTACAGTGGC	ATGATCTCGG	CTCACTGCAA	CCTCT	535

(2) INFORMATION ON SEQ ID NO. 63:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1098 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

GTGATTGAC  ATTTGAACAA  ATTAGGAAGC  TGAATCCTGC  AGCAAACCAC  AGACTCAGGA  60
ATGATTTCCC  TGATGAAAAG  ATCCCTACCC  TAAGGGAAGC  TGTTCAGAG  TGCCTAAACC  120
ATAACCTCAC  AATCTTCTTT  GATGTCAAAG  GCCATGCACA  CAAGGCTACT  GAGGCTCTAA  180
AGAAAATGTA  TATGGAATTT  CCTCAACTGT  ATAATAATAG  TGTGGTCTGT  TCTTTCTTGC  240
CAGAAGTTAT  CTACAAGATG  AGACAAACAG  ATCGGGATGT  AATAACAGCA  TTAACACACA  300
GACCTTGAG  CCTAAGCCAT  ACAGGAGATG  GGAAACCACG  CTATGATACT  TTCTGGAAAC  360
ATTTTATATT  TGTTATGATG  GACATTTTGC  TCGATTGGAG  CATGCATAAT  ATCTTGTGGT  420
ACCTGTGTGG  AATTTTCAGCT  TTCCTCATGC  AAAAGGATTT  TGTATCCCCG  GCCTACTTGA  480
AGAAGTGGTC  AGCTAAAGGA  ATCCAGGTTG  TTGGTTGGAC  TGTTAATACC  TTTGATGAAA  540
AGAGTTACTA  CGAATCCCAT  CTTGGTTCCA  GCTATATCAC  TGACAGCATG  GTAGAAGACT  600
GCGAACCTCA  CTTCTAGACT  TTCACGGTGG  GACGAAACGG  GTTCAGAAAC  TGCCAGGGGC  660
CTCATACAGG  GATATCAAAA  TACCCTTTGT  GCTAGCCCAG  GCCCTGGGGA  ATCAGGTGAC  720
TCACACAAAT  GCAATAGTTG  GTCAGTGCAT  TTTTACCTGA  ACCAAAGCTA  AACCCGGTGT  780
TGCCACCATG  CACCATGGCA  TGCCAGAGTT  CAACACTGTT  GCTCTTGAAA  ATCTGGGTCT  840
GAAAAACGC  ACAAGAGCCC  CTGCCCTGCC  CTAGCTGAGG  CACACAGGGA  GACCCAGTGA  900
GGATAAGCAC  AGATTGAATT  GTACAATTTG  CAGATGCAGA  TGTAAATGCA  TGGGACATGC  960

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ATGATAACTC  AGAGTTGACA  TTTTAAACT  TGCCACACTT  ATTTCAAATA  TTTGTACTCA  1020
GCTATGTTAA  CATGTACTGT  AGACATCAA  CTTGTGGCCA  TACTAATAAA  ATTAATAAAA  1080
GGAGCACTAA  AGGAAAAA

```

1098

(2) INFORMATION ON SEQ ID NO. 64:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1860 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

TAAGATCCTG	ACTCTGAAGC	TTCAAAGTGA	CACTGTGGAA	ATCTGAAACG	AGGGGATGTC	60
ATGAAGGCAG	CTTTTCTTTT	TCTGAGGAAA	AAATAGGCAT	GGGCTACAGG	ACTATTTAAA	120
ATGTCTCATT	TACAGTATAA	AACTCAAAGG	TAGATGTAAT	TTTACACCT	ATGAGTATTT	180
GTCCAATTTT	TGTCTCTTCC	TCACCATTGG	GTATCTATTC	TTTATATGTA	AATAAGATAA	240
GGTCATCTGA	TAGCCTTATT	CAGTCTTCAT	CATTTTCATC	ATTGTTCCCTA	TGTAGATTAT	300
TGGACATTTA	TTGTAGCACT	ACATAACTGA	TTATAAAAAT	CTGTAAATGA	ATTAGCACTT	360
TCATATTGAA	ACAAGCCTGC	TAGCCTATGT	ATAAAATAGC	AAAATGTTTG	CTGTTTATAA	420
AAAGATGTAA	TGGGGTGGGG	GGCAGGGGTA	ATTTCAAGTT	ATTAATTTAA	AAATGAACTA	480
GCAATTTTGT	ACCTGGTGAC	TTTGTGGTGC	ACTCACCTCT	GATAGTGAAT	TGAATTCGGT	540
ATGTAAAAAG	GGGTAGTGG	TATTTTCATTG	CTGCTAAAAA	TGACAACTCC	CTCTGTGTCC	600
TGTTTTTCTT	AAAGCTGTCA	GTGTACAAGT	GGGTATTTGA	ATACCAGACC	TTACTGTAAA	660
AAATAAAAAA	GGTGGTATCT	AGAGCATGTA	AATTGGATAT	AAAGTTCTGC	TCTTAAAGAG	720
TTGATCTAAG	AGTATGGCTA	AACATCTATA	TATGCAATCT	ATTAAAAGAA	CTTAATTCGG	780
CTATTATGTC	TTGATTTGAT	TGCAGTTTTT	TCCTAATTAT	AACAAATTTT	TCCTCATTGG	840
CCTGTTTTTA	ATCCTGTGCC	TAGAAGGAGT	ACAAAATGCA	CACTTTACAA	AATTGATATT	900
TAACACTTAC	CCACTCCCCT	TTCCCCATCT	CTTCTACCGC	TCTTGTTGAT	CGTGGTATCT	960
GATCTTGACT	AGATAGGCTG	AAGGCACATG	GTTCCCTCCA	AAAACCACTA	TTGATACCAC	1020
TACAAAAACA	AGCCAGCAAA	AAGATACTGT	AGAGAGGTTG	GCTTGCTTCC	CTCTCTTCC	1080
AACTGCATGT	TGAAAAATAA	GCCGTTATTG	ATCTTAAACA	TCCGTCAGAT	GAGTCATACA	1140
TTGGGTATT	TTTTATATAC	ATGTATACAC	AAAATATTTT	AAATTGAAAG	CAACATCTTA	1200
ATGGATTCAA	AACTATTACA	AGCTGTTGTC	TAAAACAGGT	GAGAAAAAAA	TTTATAACTG	1260
TAAAAACAAA	TGCACATATT	GATATTTAAA	ATGCGTAATT	AAGAAAACCC	ATTGTTGTTG	1320
TGTTTTTCTT	GTATACCAAT	AATTAAGCCA	CTACTGTTGG	CACTGTTTGG	TTTTCTATTT	1380
TAACACTGAA	GGAGTGAAAG	TATTTCTCTAT	ATTTATGAAT	TTACTACTAA	AATCTTGGA	1440
AAAAAAGAAA	AAAATTGTCT	AACGTGTGTG	GGTGAAACT	GTTAATCAAG	TGTTTCTACT	1500
CCCCCCCCGAA	AATCCCCTGA	AAGTTGGACA	CCAAGTGTAT	ACCCTAGGTT	GCTTAAAGGG	1560
ATTTCACTAT	TATATAAAGT	CAATAAAAAT	GAAGTAGTTG	TATATATGCA	ACATTGTGTA	1620
CAGAGGGGAA	ATAATGAATA	GTATTAAAGA	AACATTCTCG	TCTTCCTTTA	CCTTAATCC	1680
CCTAATACCT	AGTCTACTTT	TTAAATTTTC	AGACTTCACT	GCTTTTTGAA	TTCATAATTC	1740
TAATTTTCAC	ATTATTGTTA	ATGGAAAATC	ATATCTAATA	AAGGTTTTAG	TTATTTCCAT	1800
GCACAGTATG	AAAATTCTCA	TTTGCTGAGG	TTTTGTTTCA	AGAAAATGTA	TTGGCATGTC	1860

(2) INFORMATION ON SEQ ID NO. 66:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 205 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CRTWSILRGR MWLSTNSAAD AINPWPGRSS RPRSRAAVPH RLLHLPPVCA ELQGQQFYSL 60
 EGAPYCEGCY TDTLEKCNCTC GEPITDRMLR ATGKAYHPHC FTCVVCARPL EGTSFIVDQA 120
 NRPHCVDPYH KQYAPRCSVC SEPIMPEPGR DETVRVVALD KNFHMICYKC EDCGKPLSIE 180
 ADDNGCFPLD GHVLCRKCHT ARAQT 205

(2) INFORMATION ON SEQ ID NO. 67:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 150 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

AARALKRPFP SGPPLRDRSP SLESQSRKTP RLPEDLASGK KDYTFQRPLR RRDRKRRASR 60

VSLRVDPSDH GGPGVVADEV PHQGKCGWGR RLPGVVRPGAA GAQRQEPGSP TEGWGGGPPR120
 HVPVQPVRVS ADRPADTPAP SPSKDLLSHP 150

(2) INFORMATION ON SEQ ID NO. 68:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 55 amino acids
 (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

LLECRHHDGD VSSVGGPLQG PRVLQGGGLGV CEGAHQVASQ QGRLPRPERA GLPLT 55

(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 182 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

SVHFPAALRC ETAALLWSLR AARHHSQRT LRRARKTTTPS RGLCGAATGS GGRAECPCAW 60
IRATMVARVW SLMRFLIKGS VAGGAVYLVY DQELLGPSDK SQAALQKAGE VVPPAMYQFS120
QYVCQQTGLQ IPQLPAPPKI YFPIRDWNA GIMTVMSALS VAPSKAREYS KEGWEYVKAR180
TK 182

(2) INFORMATION ON SEQ ID NO. 70:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 25 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

PEDSGLGPHS EGRPPDCRPN KGLQK

25

(2) INFORMATION ON SEQ ID NO. 71:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 56 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

DEKNTSFLYS DVGATSMKSV LYESYTKMGR HLVNCARYLK CMFRKAFYQL RNMTYF 56

(2) INFORMATION ON SEQ ID NO. 73:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 291 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

LERLVDIKKG NTL LLQHLKR IISDLCKLYN LPQHDPVEML DQPLPAEQCT QEDVSSSEDED 60
 EEMPEDTEDL DHYEMKEEEP AEGKKSEDDG IGKENLAILE KIKKNQRQDY LNGAVSGSVQ120
 ATDRMLKELR DIYRSQSFKG GNYAVELVND SLYDWNVKLL KVDQDSALHN DLQILKEKEG180
 ADFILLNFSF KDNFPFDPPF VRVVSFVLSG GYVLGGGAIC MELLTKQGWS SAYSIESVIM240
 QISATLVKKG ARVQFGANKS QYSLTRAQQS YKSLVQIHEK NGWYTPPKED G 291

(2) INFORMATION ON SEQ ID NO. 74:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 253 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

RSVVRCLKM AAEEPQQQKQ EPLGSDSEGV NCLAYDEAIM AQQDRIQQEI AVQNPLVSER 60
 LELSVLYKEY AEDDNIYQQK IKDLHKKYSY IRKTRPDGNC FYRAFGFSL EALLDDSKEL120
 QRFKAVSAKS KEDLVSQGFT EFTIEDFHNT FMDLIEQVEK QTSVADLLAS FNDQSTSDYL180
 VVYLRLLTSG YLQRESKFFE HFIEGGRTVK EFCQQEVEPM CKESDHIHII ALAQALSVSI240
 QVEYMDRGEG GTT 253

(2) INFORMATION ON SEQ ID NO. 75:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 108 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

EKFLNMGAPL GVGLGLVFVS SIGIYVSSTY PPVAGATLYS VAMYGGGLVLF SMFLLYDTQK 60
 VIKRAEVSPM YGVQKYDPIN SMLSIYMDTL NIFMRVATML ATGGNRKK 108

(2) INFORMATION ON SEQ ID NO. 82:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

MHRDSCPLDC KVVVGNLGN GNKTELERAF GYGPLRSVW VARNPPGFAF VEFEDPRDAA 60
DAVRELDGRT LCGCRVRVEL SNGEKRSNR GPPPSWGRRP RDDYRRRSPP PRRRSPPRRS 120
FSRSRSRSL S RDRRRERSLS RERNHKPSRS FSRSRSRSS NERK 164

```

(2) INFORMATION ON SEQ ID NO. 83:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

EAALTLCHELL SSWVSLESLT LSYNGLGSNI FRLDSLRL SGQAGCRLRA LHLSDLFSPL 60
PILELTRAIV RALPLLRVLS IRVDHPSQRD NPGVPGNAGP PSHIIGDEEI PENCLEQLEM120
XISTGSPASP TAVLRSEGLG FSAAAVPG 148

```

(2) INFORMATION ON SEQ ID NO. 90:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

EDGADGAFYP DEIQRPVVRV PSWGLEDNVV CSQPARNFSSR PDGLEDSEDS KEDENVPTAP 60
 DPPSQHLRGH GTGFCFDSSF DVHKKCPLCE LMFPPNYDQS KFEEHVESHV KVCPMCSEQF 120
 PPDYDQQVFE RHVQTHFDQN VLNFD 145

(2) INFORMATION ON SEQ ID NO. 91:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 282 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

DKSSACRRNG NYSDEKKDAM YWEKRRKNNE AAKRSREKRR LNDLVLENKL IALGEENATL 60
 KAELLSLKLK FGLISSTAYA QEIQKLSNST AVYFQDYQTS KSNVSSFVDE HEPSMVSSSC120
 ISVIKHSPQS SLSDVSEVSS VEHTQESSVQ GSCRSPENKF QIIKQEPMEL ESYTREPRDD180
 RGSYTASIYQ NYMGNSFSGY SHSPPLLQVN RSSSNSPRTS ETDDGVVGKS SDGEDEQQVP240

KGPIHSPVEL KHVHATVVKV PEVNSSALPH KLRIKAKAMQ IK

282

(2) INFORMATION ON SEQ ID NO. 92:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 92 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

MASLGHILVF CVGLLTMAKA ESPKEHDPFT YDYQSLQIGG LVIAGILFIL GILIVLSRRC 60
RCKFNQQQRT GEPDEEEGTF RSSIRRLSTR RR 92

(2) INFORMATION ON SEQ ID NO. 93:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 140 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

WTGTGRGAVA IMADPDPRYP RSSIEDDFNY GSSVASATVH IRMAFLRKVY SILSLQVLLT 60
TVTSTVFLYF ESVRTFVHES PALILLFALG SLGLIFALT L NRHKYPLNLY LLFGFTLLEA 120
LTVAVVVTSM MYILSASFHT 140

(2) INFORMATION ON SEQ ID NO. 97:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 51 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

FFPLLLPLHT PVAGRNLGFP ESLGVPPFLP HPGGTPRAPG LFLLLFSFWA V

(2) INFORMATION ON SEQ ID NO. 98:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

FFLYSFPTFP PWLEGTSASL KAWGSHPSYP TREERPGPRA CFSSCFPFQQ FDH

53

(2) INFORMATION ON SEQ ID NO. 99:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

PLDCATFV FV FLNFFKPRMI SPASFSSPSS QTEFKGHFSS SFWHLQPQSG IF

52

(2) INFORMATION ON SEQ ID NO. 100:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

PFSSSVSFFG TAPSCLLGW ILVCALDRYR INTCALRTGS PRFIQSAHYR KLLCQNPBKD 60
PTPGSPSSLL TSTRVLLFF ILLFYCFCCG HYHWQSSFSP FLDIGVLSLK DSTLRLKVPK120
AA 122

(2) INFORMATION ON SEQ ID NO. 101:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 126 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

LFFFCFLFWD CAIMFIRRLD FGVCSRQIQN KYLRLENRKS TIHTKCSLQE VAVSKSRQGP 60
NSGQPLLPA LNKGCATVFY FIILLLLLS LSLAKFLFPF PGHRGPVFKR FHSEAEGAKS120
CLRSGL 126

(2) INFORMATION ON SEQ ID NO. 102:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 73 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

IDFEGKERGK GQGRDTPPLP LSWAQKLGGG RERIFTFFKL LFSEWNKLGQ GAQALSSVPH 60
TPLLRSFIQK NIS 73

(2) INFORMATION ON SEQ ID NO. 103:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

IRGRREGRV RVETPLPCPF PGPRSWGEGG KGFLHFLNCY FLNGTSWAKG PRPCPLSLTP 60
LSVHSEFKKT FLEHLLCPAY ARPTS*VCVG GLYASSSVPP CPSFTGAFGG SVGGGTFCGV 120
WSPGSPTKL SPSPVPTHLL QPPA                                     144
  
```

(2) INFORMATION ON SEQ ID NO. 104:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

CRPTIFTPRP PALGEGSTTT SPLDIPLGTG MWVPLTVRPW GEPKALTSGI AMLGGGASET 60
VGRQDILGAA PSQQGIRQGA VGDGLAQQKG TAWSGFLEIP KPHRRSHLLQ IPQRHR    116
  
```

(2) INFORMATION ON SEQ ID NO. 105:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

RMGKEALMSW RRDPPHTLSW WA

22

(2) INFORMATION ON SEQ ID NO. 109:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 165 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GAGPWEAFPD GIGRRSRRAR LPQYKRPPGG GGGGDSGRRN MAVADLALIP DVDIDSDGVF 60
 KYVLIRVHSA PRSGAPAAES KEIVRGYKWA EYHADIYDKV SGDMQKQGCD CECLGGGRIS 120
 HQSQDKKIHV YGYSMAYGPA QHAISTEKIK AKYPDYEVTW ANDGYL 65

(2) INFORMATION ON SEQ ID NO. 111:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

PSSPSLPVLR AGLRPFCDVL PGCVCVRFLC SCL

33

(2) INFORMATION ON SEQ ID NO. 112:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 31 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

ETCAGAGRCA ADGGNGSGSR VPPASRCCAL G

31

(2) INFORMATION ON SEQ ID NO. 113:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 67 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

KRAQAPAAAL QMAEMDPVAE FPQPPGAARW AEALLRCFTW LRLCQISMFL SLKCLNTRSS 60
HLGAHCR 67

(2) INFORMATION ON SEQ ID NO. 114:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 246 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

GCVAGSAGLS RKSPWTEVET ETFLGSPRYS RRVRSYWLL GLMAVRASFE NNCEIGCFAK 60
 LTNTYCLVAI GGFENFYVSF EGELSDTIPV VHASIAGCRI IGRMCVGNRH GLLVPNNTTD 120
 QELQHIRNSL PDTVQIRRV ERLSALGNVT TCNDYVALVH PDLRETEEI LADVLKVEVF 180

RQTVADQVLV GSYCVFSNQG GLVHPKTSIE DQDECLSFQV PCCGDVNEAL SDSWDVYNVS 240
 FVPETT 246

(2) INFORMATION ON SEQ ID NO. 116:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

MGYNLSPQFT QLLVSRYCPR SANPAMQLDR FIQVCTQLQV LTEAFREKDT AVQGNIRLSF 60
 EDFVTMTASR ML 72

(2) INFORMATION ON SEQ ID NO. 117:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

EHTHRCSDQL RLATVSNSVA SKREVLCPA IGH LG

35

(2) INFORMATION ON SEQ ID NO. 118:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ATLWLAKEKF ICAQPLVTLG DAPDSRQMLV HWPSSSFLLK

40

(2) INFORMATION ON SEQ ID NO. 119:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

QKRSLEFVPSH WSPWVMHQIA GRCWFIGLRP LSS

33

(2) INFORMATION ON SEQ ID NO. 120:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 161 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

LSSSRSFIST SWGAFVFFCL LSCGSLVLG FEGASTMAV FSWASRICW RSFLRFFPDS 60
 VMLARALDAR FLRWCRVISP WSITAPTTRC LRRRSRFNTR RRLNSFFFSS VRGRLIFPPG 120
 APIVAIPLQF TVRTSAQRRI RGLRPGLPRA NRNSGAGPRA I 161

(2) INFORMATION ON SEQ ID NO. 121:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 49 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

FFQSARALLQ MELTAREALL QSFFCTFFPP KDIPLGEVSR PLGRRKSGE

49

(2) INFORMATION ON SEQ ID NO. 122:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

KGALLLSKSS ETTTESEGWL QLRIF

25

(2) INFORMATION ON SEQ ID NO. 123:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

WKRFSSHLQG PSFLHPGGLL SSFAF

25

(2) INFORMATION ON SEQ ID NO. 124:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

WLLQLKPHLL AHHPPKGLPH RGAPLYSPRT RPRVAIGPRK AGAEPADPAL SGSTDRELEW 60
 NRDYGSSGGK DQPAPNGAEE EAVQTPAGVE SGAASEAPGG RGCDRPRADH AAPPEAGVQ 120
 CTCQHYTVRE EAQKTTPADP ACPEREDSHG SGSPFKASQD 160

(2) INFORMATION ON SEQ ID NO. 128:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 78 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

FFPQCQPFIF SGTHEVQLVP GTVHSLKQLK GLSPDTPATL SRMHGPGLTL SMEEVGSARG 60
 GRMVARDTES LVLGLWLS 78

(2) INFORMATION ON SEQ ID NO. 129:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 110 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

CALLPPTPSR TEP SLHSTGD SGKGAEDRQE AHRDRPTGSQ AAPEERDIQ TEESLPAPHSF 60
QDEKNLPPPP DTDAREVGGR SGKFPFPVPP RTSEPSMLNF FFIKITFIL 110

(2) INFORMATION ON SEQ ID NO. 130:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 102 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

SLPADVPCCP PPHPAQNHPC IPQGTRARVP KIDKRHTETD QLAARQPQRR ETFRQRKVSL 60
PLIPSKMRKT CRHPPTLMPG RWEEEVGNFP SQYPQERLSL QC 102

(2) INFORMATION ON SEQ ID NO. 131:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 31 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

LCQLMCPVAP HPIPHRTIPA FHRGLGQGCR R

(2) INFORMATION ON SEQ ID NO. 132:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 166 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

QFRPARCDPV	PLPTTRSVAG	LPVGRVRQLS	RPLLGPDTGS	VANIFKGLVI	LPMSLVIRN	60
QQRVIPIRRA	PLRSKIEIVR	RILGVQKFDL	GIICVDNKNI	QHINRIYRDR	NVPTDVLSP	120
QHEHLKAGEF	PQPDFPDDYN	LGDI FLGVEY	IFHQCREDED	YNDVLT		166

(2) INFORMATION ON SEQ ID NO. 133:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 244 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

FDPKLLEGKV	KEDPDQGESM	KPLTFARFYL	PILVPSAKKA	IYMDDDVIVQ	GDILALYNTA	60
LKPGHAAAFS	EDCDSASTKV	VIRGAGNQYN	YIGYLDYKKE	RIRKLSMKAS	TCSFNPGVFV	120
ANLTEWKQRN	ITNQLEKWMK	LNVEEGLYSR	TLAGSITTPP	LLIVFYQQHS	TIDPMWNVRH	180
LGSSAGKRYG	PQFVKA AKLL	HWNGHLKPWG	RTASYTDVWE	KWYIPDPTGK	FNLIRRYTEI	240
SNIK						244

(2) INFORMATION ON SEQ ID NO. 134:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

PSFIIHSNPI WLGALLWVSH CPSSILGSLR PRGGKIQLRV GGSEPCRIMK ATCFGNDLPL 60
PVV 63

(2) INFORMATION ON SEQ ID NO. 135:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

DYLRRLSSGFC QNTPLTESTE GMGVGGLGRV RLECEGSLIY AELKSPSLYV HTFVLFSRLI 60
LAIPNPLPR 69

(2) INFORMATION ON SEQ ID NO. 136:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

QPFERYFNTPL SILHFPHL SK LNLVHRVGLC MCMQEVGVDS ALGWNPP

47

(2) INFORMATION ON SEQ ID NO. 137:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

VPPCPQLREL CPGVNNQPYL CESGHCCGET GCCTYYYELW WFWLLWTVLI LFSCCCAFRH 60
 RRAKLRLQQQ QRHVEINLLA YHG 83

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

WKSQQLHRML LTRTEFWYLS TEVSTMFTCK RLRKKPLKWT GIQSSFSVTH QSDKRLVTTL 60
 PGLFSFYNSS SIHNDFVLCS IFFNPLSI 88

(2) INFORMATION ON SEQ ID NO. 140:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 21 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CYMHFLTFVK NVTIVKKCTK M

21

(2) INFORMATION ON SEQ ID NO. 141:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 58 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

MEIEQVHFPA YRQLYTDLNI FSSCLVKVKE KGFFLPQDIT FFYITSITHH CFWWKSAAE 58

(2) INFORMATION ON SEQ ID NO. 142:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

NSFLTQMMVL QNNKMAEHFH K

21

(2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

SVTKSGFLIP CHLGDFILLC CFKIQCREVV DCRGNKVNSN FEKK

44

(2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

NPPNDKVSEI QTSLSHSICEN VQPFYCSVKE PSSGSKMNSI NQRIFYTLEK KISSNILTEY 60
CKLHFSS 67

(2) INFORMATION ON SEQ ID NO. 145:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

KVHTILHFST KSSGVLCLLY KKKLYPVAGK TLSLSLLLNN WRKCSSLYKV AYKLESELVQ 60
SPFTF 65

(2) INFORMATION ON SEQ ID NO. 146:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

KIWSREQNHC EWMNCKMKK VQAKLLQVFC HFDESKMNF GYLSTLRVFS LIFCM 55

(2) INFORMATION ON SEQ ID NO. 147:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 113 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

IPEDPHIDES KAKHQAIIMS TSLRVSPSIH GYHFDTSRK KAVGNIFENT DQESLERLFR 60
 NSGDKKAEER AKIIFAIDQD VEEKTRALMA LKKRTKDKLF QFLKLRKYSI KVV 113

(2) INFORMATION ON SEQ ID NO. 148:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 88 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

MQHFAATLQA SLLSGLQRLE RDRDWKGTRT EQTGYKDSKQ FHALCCYRGE QNAFSKDLKT 60
 LPSLQERIDA DRRAWTDVMR TKENDGWR 88

(2) INFORMATION ON SEQ ID NO. 149:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

VVEGPDGHH GDAGAEVPRC LWPRSGICGR ECGLGDRWFL RVEDRQDLNR QRIQRYAQAF 60
 HIRGSEDLDK DSVEKLELGC PFSPHLSLPM PSVSRSTSR SANWERLRQG TLRRDLRGII 120
 NRGLEDGESW EYQI 134

(2) INFORMATION ON SEQ ID NO. 152:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

MKVSAALLCL LLIAATFIPQ GLAQPDAINA PVTCCYNFTN RKISVQRLAS YRRITSSKCP 60
 KEAVIFKTIV AKEICADPKQ KVVQDSMDHL DKQTQTPKT 99

(2) INFORMATION ON SEQ ID NO. 154:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

VFFFTAENWW YFHIHSVSIQ FQYPHLMRKK CFTNEGGILK LAVMLGWRKF GI

52

(2) INFORMATION ON SEQ ID NO. 155:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 25 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

FFFLQKIGG IFTFIVFLSN FSTHI

25

(2) INFORMATION ON SEQ ID NO. 156:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 40 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

ISCNVRLEKI WYLG YFQGTI KSDFCFFVKK NFFNQYCFYK

40

(2) INFORMATION ON SEQ ID NO. 157:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 66 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

ANYCIHHKL KKRTCIRRLK TRKKIQHPNM YSQEGNQFCN RTGIMNYKQE GVEKEEKKMC 60
EFKTL 66

(2) INFORMATION ON SEQ ID NO. 158:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 23 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

PCCEVLAGVG NVWKCSQQVC WGV

23

(2) INFORMATION ON SEQ ID NO. 159:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

PAVKSQVLV MCGNAVSKFA GEFDKSIKQN KKSLGIILFH DFFCSFTPEG RNLQQVVEE 60
 EGGEQVY 67

(2) INFORMATION ON SEQ ID NO. 160:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

EGEPACSGIQ ARRVTPCPSP RDASPAPASE TSLSVPATLV GGSDLIHFQV GSGPTPGPAE 60
 DRAARPSWLT LQLALGWGGR ELMSVASLSW GFPACPVVSC PRCYRGCA 108

(2) INFORMATION ON SEQ ID NO. 161:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

FCSTTSSVAL HQKEGMGYSR

20

(2) INFORMATION ON SEQ ID NO. 162:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 61 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

IPGLKYFVGI AYYIILADEP QDNGYRHTHT YHTKSQLLK SGLGIRLLCP VKNSCTEVIV 60
T 61

(2) INFORMATION ON SEQ ID NO. 163:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 22 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

LMNLRTTATD THIHTRTQNL SC

22

(2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

TSGQRLQHT YIHAHKISAV EEAWNQTSV SSKKLLH

(2) INFORMATION ON SEQ ID NO. 165:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

TVPFVSASG FHLIFFALPI LFQPVAKNHE TRQWKHRHRR RGPSCALKAG KTASGAGEVV 60
RCLSEQSVAI SR 72

(2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

QISTSEEVLT FSMLHRNWYN MPSVY

25

(2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

LKLLAWSYLH SFCVLFASCI

20

(2) INFORMATION ON SEQ ID NO. 170:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

LLACCTETGI TCLQYTNTHM LSFVLFWQLT RS

32

(2) INFORMATION ON SEQ ID NO. 171:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 50 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

IALSCCFNVV HTIASQTCYS SVICSVVTKV TGLVLFAQFL RLVCFHLIN

50

(2) INFORMATION ON SEQ ID NO. 172:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 51 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

EHYTIGFQYC THKIHTCVQK VSSSRLVIPF TWKINEGNLY ILYKNKSKFI Y

51

(2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 239 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

LFIFHRNNTN NWREIPENLM DQYSEVNAIS TACSNGVPEC EEMVSGLFKQ WMENPNNNPI 60
 HPNLRSTVYC NAIQAQGGEEE WDFAWQFRN ATLVNEADKL RAALACSKEL WILNRYLSYT 120
 LNPDLIRKQD ATSTIISITN NVIGQGLVWD FVQSNWKKLF NDYGGGSFSF SNLIQAVTRR 180
 FSTEYELQQL EQFKKDNEET GFGSGTRALE QALEKTKANI KWVKENKEVV LQWFTENSK 239

(2) INFORMATION ON SEQ ID NO. 183:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 109 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

YANQSSSLRF KIKYKLLCFS THSGSIVPEP DCYFFILNII FPHLICLPLI HRHLEKEMGG 60
 CLLSLSLCFV PVVRLAASVA RWAWLEPWVR QVAGGDRERL RGKWWHLLL 109

(2) INFORMATION ON SEQ ID NO. 184:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

SLFLSSTGVS APLQGQSKSL HPEPPPIPVH FSR

33

(2) INFORMATION ON SEQ ID NO. 185:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

HSFSARLEFL HLCRGKVSPC TLNHPPFLFI SADNDGGGGV SIVLRV

46

(2) INFORMATION ON SEQ ID NO. 186:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```

VEGTCSDGVF SGFLAPGCAV HRPHRPWPQH PQQGQWKCQS SKCHHFPLSL SLSPPATCLT 60
HGSNQAHRAT DAASLTGTHK QREDRNRHPP ISFSKCLWMR GRQIR 105

```

(2) INFORMATION ON SEQ ID NO. 187:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```

RGHAVTEYLV GLLLLAVQFT GPTGLGPSIP SRDSGSVRV NATTSLSASP CPRQPPASPT 60
ALTKPTEQLT LPV 73

```

(2) INFORMATION ON SEQ ID NO. 188:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

MFFIFFMLSI QALFHGQQVI FHNVDLPK

28

(2) INFORMATION ON SEQ ID NO. 189:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 65 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ELNTAILWLL LVFLWYVVWE CLWNYQYLKF SKEPWKSITL NESLSLYMNY VLKFDQLSLR 60
 KKTVI 65

(2) INFORMATION ON SEQ ID NO. 190:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 30 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

CFSFFSCYLS KHCSMVSKSY FIMWIFQNNY

30

(2) INFORMATION ON SEQ ID NO. 191:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

FFVTNVFY LFINKKCIVQ ALYPNPSTQK KINNRPWMAQ T

41

(2) INFORMATION ON SEQ ID NO. 192:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

YKPFIPQVL RKRLTTDPGW HRHNLFQVI

29

(2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

SSHMVTNTYD FFRNIIRRL NLLLQQQKFN PLN

33

(2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

TPLRKEVLKS KMGKSEKIAL PHGQLVHGIH LYEQPKINRQ KSKYNLPLTK ITSAKRNENN 60
 FWQDSVSSDR IQKQEKKPFK NTENIKNSHL KKSAPLFEVS QKENYAGAKF SDPPSPSVLP 120
 KPPSHWMGST VENSQNREL MAVHLKTLK VQT 153

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 304 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```

SLYYYGIRDL  ATVFFYMLVA  IIIHAVIQEY  MLDKINRRMH  FSKTKHSEFN  ESGQLSAFYL  60
FACVWGTFIL  ISENYISDPT  ILWRAYPHNL  MTFQMKFFYI  SQLAYWLHAF  PELYFQKTKK  120
EDIPRQLVYI  GLYLFHIAGA  YLLNLNHLGL  VLLVLHYFVE  FLFHISRLFY  FSNEKYQKGF  180
SLWAVLFVLG  RLLTLILSVL  TVGFGGLARAE  NQKLDFTGN  FNVLAVRIAV  LASICVTQAF  240
MMWKFINFQL  RRWREHSAFQ  APAVKKKPTV  TKGRSSKKG  ENGVNGTLTS  NVADSPRNKK  300
EKSS                                              304

```

(2) INFORMATION ON SEQ ID NO. 201:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 198 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```

KMTTAARPTF  EPARGGRGKG  EGDLSQLSKQ  YSSRDLPST  KIKYRQTTQD  APEEVRNRDF  60
RRELEERERA  AAREKNRDRP  TREHTTSSSV  SKKPRLDQIP  AANLDADDPL  TDEEDEDTEE  120
ESDDDDTAAL  LAELEKIKKE  RAEKGQGP  GPRAKKALRG  GRVSFWENIG  WAGNPFPLIL  180
SLAHSKLLAD  FEKFERRV

```

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 55 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

VLIFLVFLLD GKAVGINRGQ RLMLEWPVEV VEQSSHLLSG AVSGWVYLKA TKCFG

55

(2) INFORMATION ON SEQ ID NO. 203:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 66 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

SPGFFLSLPF STGXAWASSS CHPSRKAPAP SCLPAACIQG QSSGLQTGLV PPPLQGMGVG 60
GAFKK 66

(2) INFORMATION ON SEQ ID NO. 204:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 161 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

HLGYGKLLWC VVGFLFSFLS FFSPFSLLAFF SFPFSPSLAK LGPHPHVILL GRRPLHLVCR 60
QHASKARAQA CRLGWCLLRF RVWELVKGLS KNNKKKKVKS LVASIHSDPG RQQGFVDLDS 120
LGMSSCQPGQ DPGLPRAEAL PATRIPPLWG LCVQRSGSET S 161

(2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

DLVLFIVEH TYQGEVLHTQ LQIIFGKKAV KKIKLQLL

37

(2) INFORMATION ON SEQ ID NO. 206:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

ENYFAFSVNL RSVLNKVQSS ARPFP SLMSA LG

32

(2) INFORMATION ON SEQ ID NO. 207:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

CMLQINLYFF PLGFSKNTTT STPNEHGTCL FLPLLIYSRF SSVFFSNAAF SCSSGLLSGS 60
IVAKDSIRST LHSDVKHSHC LDSSSFSSN SITDKASVLT DE 102

(2) INFORMATION ON SEQ ID NO. 208:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 34 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

VLFSKEYVID LQVSSRISAK ASGSACSSSK SINP

34

(2) INFORMATION ON SEQ ID NO. 209:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 43 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

VAHWQGDQKH YFHTCVMILF FLRESHSVAR LGVQWHDLS LQP

43

(2) INFORMATION ON SEQ ID NO. 210:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 204 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```

DLTFEQIRKL NPAANHRLRN DFPDEKIPTL REAVAECLNH NLTIFFDVKG HAHKATEALK 60
KMYMEFPQLY NNSVVC SFLP EVIYKMRQTD RDVITALTHR PWSLSHTGDG KPRYDTFWKH 120
FIFVMM DILL DWSMHNILWY LCGISAFLMQ KDFVSPAYLK KWSAKGIQVV GWTVNTFDEK 180
SYYESHLGSS YITDSMVEDC EPHF 204

```

(2) INFORMATION ON SEQ ID NO. 214:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 33 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

```

SFKVTLWKSE TRGCHEGSFS FSEEKIGMGY RTI

```

33

(2) INFORMATION ON SEQ ID NO. 215:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 61 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

NSKVDVIFTP MSICPISVSS SPLGIYSLYV NKIRSSDSLI QSSSFSSLFL CRLLDIYCST 60
T 61

(2) INFORMATION ON SEQ ID NO. 216:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 24 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

PMYKIAKCLL FIKRCNGVGG RGNF

24

(2) INFORMATION ON SEQ ID NO. 217:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1880 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

CGCCGGGGGC	CGGGGGCGGC	CCAGGGGGGG	GCCCGGGGCC	GGGGCCCTGC	CTGAGGCGAG	60
AGCTGAAGCT	GCTCGAGTCC	ATCTTGCCAC	CGCGGCCACG	AGCGCTTCCG	CATTGCCAGC	120
GCCTGCCTGG	ACGAGCTGAG	CTGCGAGTTC	CTGCTGGCTG	GGGCCGGAGG	GGCCGGGGCG	180
GGGGCCGCGC	CCGGACCGCA	TCTCCCCCCA	CGGGGGTCGG	TGCCTGGGGA	TCCTGTCCGC	240
ATCCACTGCA	ACATCACGGA	GTCATACCCT	GCTGTGCCCC	CCATCTGGTC	GGTGGAGTCT	300
GATGACCCTA	ACTTGGCTGC	TGTCTTGAG	AGGCTGGTGG	ACATAAAGAA	AGGGAATACT	360
CTGCTATTGC	AGCATCTGAA	GAGGATCATC	TCCGACCTGT	GTAAACTCTA	TAACCTCCCT	420
CAGCATCCAG	ATGTGGAGAT	GCTGGATCAA	CCCTTGCCAG	CAGAGCAGTG	CACACAGGAA	480
GACGTGTCTT	CAGAAGATGA	AGATGAGGAG	ATGCCTGAGG	ACACAGAAGA	CTTAGATCAC	540
TATGAAATGA	AAGAGGAAGA	GCCAGCTGAG	GGCAAGAAAT	CTGAAGATGA	TGGCATTGGA	600
AAAGAAAAC	TGGCCATCCT	AGAGAAAATT	AAAAAGAACC	AGAGGCAAGA	TTACTTAAAT	660
GGTGCAGTGT	CTGGCTCGGT	GCAGGCCACT	GACCGGCTGA	TGAAGGAGCT	CAGGGATATA	720
TACCGATCAC	AGAGTTTCAA	AGGCGGAAAC	TATGCAGTCG	AACTCGTGAA	TGACAGTCTG	780
TATGATTGGA	ATGTCAAAC	CCTCAAAGTT	GACCAGGACA	GCGCTTTGCA	CAACGATCTC	840
CAGATCCTCA	AAGAGAAAGA	AGGAGCCGAC	TTCATTCTAC	TTAACTTTTC	CTTTAAAGAT	900
AACTTTCCCT	TTGACCCACC	ATTTGTCAGG	GTTGTGTCTC	CAGTCCTCTC	TGGAGGGTAT	960
GTTCTGGGCG	GAGGGGCCAT	CTGCATGGAA	CTTCTCACCA	AACAGGGCTG	GAGCAGTGCC	1020
TACTCCATAG	AGTCAGTGAT	CATGCAGATC	AGTGCCACAC	TGGTGAAGGG	GAAAGCACGA	1080
GTGCAGTTTG	GAGCCAACAA	ATCTCAATAC	AGTCTGACAA	GAGCACAGCA	GTCTTACAAG	1140
TCCTTGGTGC	AGATCCACGA	AAAAACGGC	TGGTACACAC	CCCCAAAAGA	AGACGGCTAA	1200
CCCTGGAGTA	TCACCCTTCC	TCCCTCCCCA	GGCACCCTG	GACCAATTAC	CTTTGAATGC	1260
TGTATTTGGA	TCTCAGCTG	CCTCTGTGGT	TCCCTCCCTC	ATTTTTCTCTG	GACGTGATAG	1320
CTCTGCCTAT	TGCAGGACAA	TGATGGCTAT	TCTAAACGCT	AAGGAAAAAA	AACAAACACA	1380
GAAGTGTTC	AAGTACTCAA	GACTGACTTA	CAGACCAACC	AACCACCTTG	CTGGAACCCT	1440
TGCTAGCAGG	CATTCTTATA	AAAGAAACTT	TCGAGCCTCC	TTATATTGCT	GGAAACTCAG	1500
CTGTGCTCCA	GACTAGAGCC	TCCTTACCTA	TGCTATGGAT	TTTTAATTTA	TTTTCTCTTA	1560
TTTCATGTAC	ACTGCTTTTT	TTGGTTACAG	TGTATGATGG	ATGTGTATGA	AAAAATGTAT	1620
TCTTTGGGAA	AACAATTACA	GTTTGTTAAT	TTGGAAAAAA	AAAAAATGAC	TCATCTTTAT	1680
TTTTATTTCG	ACATCCCACC	CCATCCCCTG	GAAGTACTTG	GGGAGGTGGG	GAGGGGTACG	1740
AGTCCACTGT	TGGCTTG GTA	GGAGATGAGA	GGCCGCATTT	GCTGCTTAAG	CAAGGGGAAC	1800
TGGGGCTGAG	CACACACCGG	GGTGCCCCCG	GATTTTTCTC	CAAGGGCTCT	GGAGCAACGG	1860
CACCGGCCCC	TTGGGATGCA					1880

(2) INFORMATION ON SEQ ID NO. 218:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1024 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

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GCGGTCGGTA GTGCGGCGCT GTTTAAAGAT GGCGGCGGAG GAACCTCAGC AGCAGAAGCA 60
GGAGCCGCTG GGCAGCGACT CCGAAGTGTT AACTGTCTGG CCTATGATGA AGCCATCATG 120
GCTCAGCAGG ACCGAATTCA GCAAGAGATT GCTGTGCAGA ACCCTCTGGT GTCAGAGCGG 180
CTGGAGCTCT CGGTCCTATA CAAGGAGTAT GCTGAAGATG ACAACATCTA TCAACAGAAG 240
ATCAAGGACC TCCACAAAAA GACTCGTAC ATCCGCAAGA CCAGGCCTGA CGGCAACTGT 300
TTCTATCGGG CTTTCGGATT CTCCCACTTG GAGGCACTGC TGGATGACAG CAAGGAGTTG 360
CAGCGGTTCA AGGCTGTGTC TGCCAAGAGC AAGGAAGACC TGGTGTCCCA GGGCTTCACT 420
GAATTCACAA TTGAGGATTT CCACAACACG TTCATGGACC TGATTGAGCA GGTGGAGAAG 480
CAGACCTCTG TCGCCGACCT GCTGGCCTCC TTCAATGACC AGAGCACCTC CGACTACCTT 540
GTGGTCTACC TGCGGCTGCT CACCTCGGGC TACCTGCAGC GCGAGAGCAA GTTCTTCGAG 600
CACTTCATCG AGGGTGGACG GACTGTCAAG GAGTTCTGCC AGCAGGAGGT GGAGCCCATG 660
TGCAAGGAGA GCGACCACAT CCACATCATT GCGCTGGCCC AGGCCCTCAG CGTGTCCATC 720
CAGGTGGAGT ACATGGACCG CGGCGAGGGC GGCACCACCA ATCCGCACAT CTTCCCTGAG 780
GGCTCCGAGC CCAAGGTCTA CCTTCTCTAC CGGCCTGGAC ACTACGATAT CCTCTACAAA 840
TAGGGCTGGC TCCAGCCCGC TGCTGCCCTG CTGCCCCCCT CTGCCAGGCG CTAGACATGT 900
ACAGAGGTTT TTCTGTGGTT GTAAATGGTC CTATTTTACC CCCTTCTTCC TGTCACATGA 960
CCCCCCCCCA TGTTTTATTA AAGGGGGTGC TGGTGGTGAA AAAAAAAAAA AAAAAAAAAA 1020
AAAA

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1024

(2) INFORMATION ON SEQ ID NO. 219:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2383 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

CCCTTCATTA	AAGCCCTCCT	AAATATAACT	CTTCTGTATC	AAAGGACTTA	CAAATGTCTC	60
AAGAAAGTAA	TGGTGTAGCA	GTGTAAGAGA	AGTAAAAGTC	TGCTAGGGGA	AACTAATGAA	120
GCATTTTCCT	CATTACACTT	TTGGGTTGAT	ATATTTTCATT	AAGACAGAAC	TAGTTCTGTT	180
TTGCTTTGCT	TTTTAGTGCT	TAGTCTGAGA	GGCAATGCGA	GAAACCAAAA	GTCTTAGGAG	240
AAAAACTGCT	TTCATAAATTT	CCAGTGTAAG	CCACAAAGAA	GCTTTTCTAT	AAAGGCTTGA	300
AAGCTTGAAG	AGGTGACAAG	AGCAAGCTGT	ATTCAATTAG	ACAGTTCAAT	AAATATGCAA	360
AAATAAAAAA	ACACTTATCA	ATCATGAGTA	TACTGTTTGT	ATTCTGGAAA	AAGCAACATA	420
TTTCATGCTT	TGAATATTTT	CTCTTGAGAA	TAGTTTTTAA	GTTATTTCCCT	TTTGTAACAT	480
TCAAAAGTAA	AACACACATA	TATAATTCCA	TCAAGGATTC	TCTGTATGAT	TAACATTCTG	540
TACAAGTCAA	ACATGACCAC	ATCTATATTG	GAAAGAGAGC	ACTGAGAAGC	AACAGCAGGA	600
GAATGCATCA	CCTGTGCCTG	TTTCAGGATG	AACAGTTTTG	TTAAGTTCAG	CAGATGAATG	660
TAACAATGAC	CACTTGTTTC	CAAATACCCA	GATGTTTCTT	ACTGGCTCCT	CACTAATCAA	720
TAACACAAGT	GCTAAGTTCT	AAGTATTTAA	AAAAACAAAA	GACTGCAGGT	GACTCCTTCT	780
CTCTGGTCCC	TTTACCAAAG	CTCCAAATCA	CTTATGACAT	TAATTACAAT	ATTCTGCACT	840
CCAAAAAAT	ATGCAAACAC	AGGTTTGCTA	AATTTTAGTT	ACTCAGTGAA	CCTACTAAAT	900
TTTAAAGTAG	AAAAAAGACT	TACATTCTCA	TGACACAAAC	TTTAGTTTTT	ACATTCACCA	960
AAACATTTTA	AAATCACTCA	AACATGAGAA	TTGAAAATGT	GTGTGCTTAT	TTGGGAGAGG	1020
ATTACTGCAT	TTATTCTCCA	GAAAAAAGG	CAGACCTGAG	GCATCACAAT	ACCGGAACAT	1080
TTAAATATGA	TGACATGTTT	CTTATCTTCT	AAACTTCAAC	GAAAGCTGCT	TGTACAAACT	1140
ATTTAATGCA	TATCTGCCCC	ATTAAACAAG	ATATTTGATG	TAGCAGAGAA	GCCAGAAGCT	1200
GAGTCACTTC	ATTTCTTTCT	GTTGCCTCCA	GTTGCCAGCA	TAGTTGCAAC	TCGCATAAAT	1260
ATATTTAATG	TATCCATGTA	GATACTCAGC	ATCGAGTTAA	TGGGATCATA	TTTTTGAACT	1320
CCATACATTG	GTGATACTTC	TGCACGCTTG	ATTACTTTCT	GGGTATCATA	CAGAAGGAAC	1380
ATGCTGAAAA	GAACATAATCC	ACCGTACATT	GCCACTGAGT	AAAGAGTGGC	ACCAGCCACG	1440
GGTGGTAGGT	GGAAGAAACA	TAGATCCCAA	TGAGGACACA	AAGACGAGAC	CCAGGCCAC	1500
TCCCAGGGGT	GCACCCATGT	TCAGAAACTT	TTCCTGAGGC	GCACACATGG	CCACAGTGGA	1560
GAGGCCTCCC	ACAATGCCAG	CTGTGTACCA	TGCAGCTCTG	ATGAGAAGAG	GACCCCTAA	1620
TATTGTCAGA	GGAGCCACCA	CTGCACCCAT	CACACCAGAA	TGTAGCAACC	AAGCAAGATG	1680
CTTTGGGCCT	GGGCTCTGGT	CATATGGTAT	TGATCGTACC	AGCATTCCAG	CTCCAACCAT	1740
GGCTGCAAAG	GTCACACCAA	TTGTCACCCA	AGAGCCTCTC	ATCATGAAGT	TCATGAGAAC	1800
AGGCGTTCTG	CTGATTGCTA	TGGCAGACAA	AGCTGTTAAA	CCAATACTCC	CTGCTAAGTA	1860
CATATAGGTG	GAATGAATTC	TATCCTTGAC	ATACTGAGGC	CAAATTACAG	CCTTTTCAAT	1920
AGCTCCAATC	TCATTAGACA	GTCCCAAGCC	ATAGTAGCAC	AATGCTCCAA	GACCAACAGC	1980
AGCCCTCCA	GCAACAAACC	ATCTTCCCAT	CTGATCAATT	TTAAATATTT	TTTCCATCGA	2040
TGGTTCCAAT	GCTGCCTCTT	TGAGTTCTTG	GCCAGTTCTC	CCACGCCGGA	TCCCAATTCT	2100
TGTTTTGGTG	GCATATTCCC	TGCTAGGTGT	TAACAGCCAT	TGATTCTTCG	TGATGGAATT	2160
CTTCACAACA	GGGGAGGCCT	TGGTGAAAGC	TGGGTGAAA	ACCCTAGAAG	GTAGTGTCGG	2220
GAGACACACC	AGCCTTGCAG	CCAACATGGT	GGTGGTGCAC	CAGGTCTACC	GAGCAGATCT	2280
GAAATGCTCG	GTCCCCGGTC	ACCTTCGCCT	CGCAGTTTCC	CTTCCGGGCC	CCTAGCGTCG	2340
GCCTCAAAGA	GCACAGTTCC	TCCGGCGCAC	TGCATGTCGC	AAC		2383

(2) INFORMATION ON SEQ ID NO. 220:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3210 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

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GCAAGGCCTA CTGTCGGCTG GGAGGGGAGG TGTAGCCGGT CTTTGGGGGT AGGCGGTAGT 60
GGCGGAAGAG GTTCGGCGGC TGATGGCGGA TCAGGATCGG AAGCCTGCGT AACTTTCTCC 120
CTTGATCCGG GAGTCTTTCC ACTGGATTCA CAATGACATC CTTTCAAGAA GTCCCATTGC 180
AGACTTCCAA CTTTGCCCAT GTCATCTTTC AAAATGTGGC CAAGAGTTAC CTTCTAATG 240
CACACCTGGA ATGTCATTAC ACCTTAACTC CATATATTCA TCCACATCCA AAAGATTGGG 300
TTGGTATATT CAAGGTTGGA TGGAGTACTG CTCGTGATTA TTACACGTTT TTATGGTCCC 360
CTATGCCTGA ACATTATGTG GAAGGATCAA CAGTCAATTG TGTACTAGCA TTCCAAGGAT 420
ATTACCTTCC AAATGATGAT GGAGAATTTT ATCAGTTCTG TTACGTTACC CATAAGGGTG 480
AAATTCGTGG AGCAAGTACA CCTTCCAGT TTCGAGCTTC TTCTCCAGTT GAAGAGCTGC 540
TTACTATGGA AGATGAAGGA AATTCTGACA TGTTAGTGGT GACCACAAAA GCAGGCCTTC 600
TTGAGTTGAA AATTGAGAAA ACCATGAAAG AAAAAGAAGA ACTGTTAAAG TTAATTGCCG 660
TTCTGGAAAA AGAAACAGCA CAACTTCGAG AACAGTTGG GAGAATGGAA AGAGAACTTA 720
ACCATGAGAA AGAAAGATGT GACCAACTGC AAGCAGAACA AAAGGGTCTT ACTGAAGTAA 780
CACAAAGCTT AAAAATGGAA AATGAAGAG TTAAGAAGAG GTTCAGTGAT GCTACATCCA 840
AAGCCCATCA GCTTGAGGAA GATATTGTGT CAGTAACACA TAAAGCAATT GAAAAAGAAA 900
CGAATTAGA CAGTTTAAAG GACAACTCA AGAAGGCACA ACATGAAAGA GAACAACCTG 960
AATGTCAGTT GAAGACAGAG AAGGATGAAA AGGAACTTTA TAAGGTACAT TTGAAGAATA1020
CAGAAATAGA AAATACCAAG CTTATGTCAG AGGTCCAGAC TTTAAAAAAT TTAGATGGGA1080
ACAAAGAAAG CGTGATTACT CATTTCAAAG AAGAGATTGG CAGGCTGCAG TTATGTTTGG1140
CTGAAAAGGA AAATCTGCAA AGAAGCTTCC TGCTTACAAC CTCAAGTAAA GAAGATACTT1200
GTTTTTTTAAA GGAGCAACTT CGTAAAGCAG AGGAACAGGT TCAGGCAACT CGGCAAGAAG1260
TTGTCTTTCT GGCTAAAGAA CTCAGTGATG CTGTCAACGT ACGAGACAGA ACGATGGCAG1320
ACCTGCATAC TGCACGCTTG GAAAACGAGA AAGTGAAAAA GCAGTTAGCT GATGCAGTGG1380
CAGAACTTAA ACTAAATGCT ATGAAAAAAG ATCAGGACAA GACTGATACA CTGGAACACG1440
AACTAAGAAG AGAAGTTGAA GATCTGAAAC TCCGTCTTCA GATGGCTGCA GACCATTATA1500
AAGAAAAAT TAAGGAATGC CAAAGGCTCC AAAACAAAT AAACAACTT TCAGATCAAT1560
CAGCTAATA TAATAATGTC TTCACAAAGA AAACGGGGA TCAGCAGAAA CTGAATGATG1620
CTTCAGTAAA CACAGACCCA GCCACTTCTG CCTCTACTGT AGATGTAAAG CCATCACCTT1680
CTGCAGCAGA GGCAGATTTT GACATAGTAA CAAAGGGGCA AGTCTGTGAA ATGACCAAAG1740
AAATTGCTGA CAAAACAGAA AAGTATAATA AATGTAAACA ACTCTTGCAG GATGAGAAAG1800
CAAAATGCAA TAAATATGCT GATGAACTTG CAAAATGGA GCTGAAATGG AAAGAACAAG1860
TGAAAATTGC TGAAAATGTA AACTTGAAC TAGCTGAAGT ACAGGACAAT TATAAAGAAC1920
TTAAAGGAG TCTAGAAAAT CCAGCAGAAA GGAAAATGGA AGATGGAGCA GATGGTGCTT1980
TTTACCCAGA TGAAATACAA AGGCCACCTG TCAGAGTCCC CTCTTGGGGA CTGGAAGACA2040
ATGTTGTCTG CAGCCAGCCT GCTCGAACT TTAGTCGGCC TGATGGCTTA GAGGACTCTG2100
AGGATAGCAA AGAAGATGAG AATGTGCCTA CTGCTCCTGA TCCTCCAAGT CAACATTTAC2160

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GTGGGCATGG GACAGGCTTT TGCTTTGATT CCAGCTTTGA TGTTACAAG AAGTGTCCTCC2220
TCTGTGAGTT AATGTTTCCT CCTAACTATG ATCAGAGCAA ATTTGAAGAA CATGTTGAAA2280
GTCACCTGGAA GGTGTGCCCC ATGTGCAGCG AGCAGTTCCC TCCTGACTAT GACCAGCAGG2340
TGTTTGAAAG GCATGTGCAG ACCCATTTTG ATCAGAATGT TCTAAATTTT GACTAGTTAC2400
TTTTTATTAT GAGTTAATAT AGTTTAGCAG TAAAAA AAAA AAAAAC CACACCTAAA2460
ATAGACCACT GAGGAGACCA TAGAGCGGAT GCTTTCATGC ACCCTTTACT GCACTTTCTG2520
ACCAGGAGCT ACTTTGAGTT TGGTGTTACT AGGATCAGGG TCAGTCTTTG GCTTATCAAT2580
AAATTTTAAT CTCTGTAAAT CTTACCTGCT TAAAAA GTTCTTGTGT GTTCGTATCT2640

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TTATTTATTC CCTAGTTTGC AGAACTGTCT GAATAAAGGA TACAAGGATT ATTTCAATGT2700
TACTGCACTG AAAAACGTGT ATGTATTAGT GTGCTAGATT ATTTAGCAGA ATATTCACAA2760
GTTTCTGTTG ACCTTGTTGA TTGAGCATGA CTACTAAATA TTATGTAATA AAAAGCATT2820
GTCATAACAG TCTTATGAAG TAGTTCTTCG AATATAGAAA GTTCTATAAT TTAGCCCATG2880
AAATGATAGG TTTTAAATTT TCAGAAATGG AGCTGCATGT AGAATGAGAT CACATGCTTT2940
TATATGTGAA ATATTGGTTT TAGCAATTAA CAGAAGGCAT ACTTTGCTAA TTTTATGGCA3000
AAATTTTAGA ATAACCTGAA TGATTATTTT TAACTATCT TGAAGTTGTA TGTATATATC3060
CTAATGGGGA AATGGGGCAA GGGATTGTCA GTATAATTGT TTTCCCGATT AAATGGTCCC3120
CATAACCAGG GGGTGTTTGT GGCATAAAAA TCCATAGGGT ATATAGCAGG ACCTTTTTTG3180
CATTTCCCTG TGGGGATTTA ATTTGGAATT

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3210

(2) INFORMATION ON SEQ ID NO. 221:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1030 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

```

CCGCTTTCTC CGCCCAGCTG GAATTTTGA AGCGAGAAAA TCGACTCGCT CCGTGTTTCGC 60
CCGCCGACGC CGCACGGTTG CTGGGGCTGG GCTCTTCCTC GCGGAAGTGG GGAGGAGGCG 120
GTTGCGGTTA GTGGACCGGG ACCGGTAGGG GTGCTGTTGC CATCATGGCT GACCCCGACC 180
CCCGGTACCC TCGCTCCTCG ATCGAGGACG ACTTCAACTA TGGCAGCAGC GTGGCCTCCG 240
CCACCGTGCA CATCCGAATG GCCTTTCTGA GAAAAGTCTA CAGCATTCTT TCTCTGCAGG 300
TTCTCTTAAC TACAGTGAAT TCAACAGTTT TTTTATACTT TGAGTCTGTA CGGACATTG 360
TACATGAGAG TCCTGCCTTA ATTTTGCTGT TTGCCCTCGG ATCTCTGGGT TTGATTTTGG 420
CGTTGACTTT AAACAGACAT AAGTATCCCC TTAACCTGTA CCTACTTTTT GGATTTACGC 480
TGTTGGAAGC TCTGACTGTG GCAGTTGTTG TTACTTTCTA TGATGTATAT ATTATTCTGC 540
AAGCTTTCAT ACTGACTACT ACAGTATTTT TTGGTTTGAC TGTGTATACT CTACAATCTA 600
AGAAGGATTT CAGCAAATTT GGAGCAGGGC TGTTTGCTCT TTTGTGGATA TTGTGCCTGT 660
CAGGATTCTT GAAGTTTTTT TTTTATAGTG AGATAATGGA GTTGGTCTTA GCCGCTGCAG 720
GAGCCCTTCT TTTCTGTGGA TTCATCATCT ATGACACACA CTCACTGATG CATAAACTGT 780
CACCTGAAGA GTACGTATTA GCTGCCATCA GCCTCTACTT GGATATCATC AATCTATTCC 840
TGCACCTGTT ACGGTTTCTG GAAGCAGTTA ATAAAAAGTA ATTAAAAGTA TCTCAGCTCA 900
ACTGAAGAAC AACAAAAAAA ATTTAACGAG AAAAAAGGAT TAAAGTAATT GGAAGCAGTA 960
TATAGAAACT GTTTCATTAA GTAATAAAGT TTGAAACAAT GATTAAAAAA AAAAAAAAAA1020

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(2) INFORMATION ON SEQ ID NO. 222:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1216 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

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TCTGTTCTGT GGACAACTGT TACTGTTCTT CCGTGGCCAA CCATGGCGGC CACCAGCCCT 60
ACCCCGCTC CGGCCACTTT CCCTGGACAG TGCCCTCGCA GGAGTACTCA CACCCGCTCC 120
CGCCACACC CTCCGTCCCC CAGTCCCTTC CCAGCCTGGC GGTCAGAGAC TGGCTTGACG 180
CCTCCAGCA GCCCGGCCAC CAGGATTTCT ACAGGGTGTA TGGGCAGCCG TCCACCAAAC 240
ACTACGTGAC GAGCTAACGC CACGCAGGCG GCGGGGCGCT GGGGAATCTT CCTCCCCAGC 300
CCCCGGGCTC GGGAGTTATG CATCCAGAGA CCTGCCCTTC TACCTTCCTC GCCTCCCCTC 360
TTCCTCATTC CATTGCCCCA GGTCTTTTCC TTTTGGATTT TGTTTTGGTT TTGGCTTTGT 420
TTTTGATTTT TTTTATTAT GAATCTCTTG GACGCAGAGG TGACAGTGGG AGCTGGCCTG 480
GGCCAGGACG GCAGGTGGCC CTGGAGATGG GAAAGTGTCT GTGTCGAGGC GCTGAGCTCT 540
CTCTCTGTTT CTCCTTTTTT CCTCTACTCC TTCCCCTTCA CACCCCGTG GCTGGAAGGA 600
ACCTCGGCTT CCCTGAAAGC TTGGGGGTCC CACCCTTCTT ACCCCACCCG GGAGGAACGC 660
CCAGGGCCCC GGGCTTGTTT CTCCTCTTGT TTTCTTTTG GGCAGTTTGA TCACTGATCG 720
AGTAAGGAAT GACCTTTAGA TTGTGCGACT TTTGTTTTTG TTTTTTTAAA TTTTTTTAAA 780
CCAAGAATGA TTTCTCTGC TTCCTTCTCC TCACCATCTT CCCAGACGGA GTTCAAAGGC 840
CACTTCTCAA GCAGCTTTTG GCACCTTCAG CCTCAGAGTG GAATCTTTTA AAGACAGGAC 900
CCCTATGTCC AGGAAAGGGG AAAAGGAACT TTGCCAATGA TAGTGACCAC AGCAAAAGCA 960
ATAAAATAAT AAAATAAAAA ACAATAGCAC AGCCCTTGTT GAGGTCAGCA GGGAGGAGGG1020
GCTGCCCCGA GTTGGGTCCT TGCCTGGATT TTGACACAGC AACTTCCTGT AGTGAGCACT1080
TTGTATGAAT CGTGGACTTC CTGTTCTCAA GGCGCAGGTA TTTATTCTGT ATCTGTCTAG1140
AGCACACACC AAAATCCAAC CTTCTAATAA ACATGATGGC GCAGTCCCAA AAAAAAGAAA1200
CAGAAGAAGA AAAGGG

```

(2) INFORMATION ON SEQ ID NO. 223:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2369 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

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CGGGCGCCCCG  GGCCAGAGTC  CGGCCGGAGC  GGAGGAGCCC  GGCCCCAGGG  ACAGCTCGGC  60
CGTCATTACT   CAGATCAGCA  AGGAGGAGGC  TCGGGGCCCCG  CTGCGGGGCA  AAGGTGACCA  120
GAAGTCAGCA   GCTTCCCAGA  AGCCCCGAAG  CCGGGGCATC   CTCCACTCAC  TCTTCTGCTG  180
TGTCTGCCGG   GATGATGGGG  AGGCCCTGCC  TGCTCACAGC   GGGGCGCCCC  TGCTTGTGGA  240
GGAGAAATGGA  GCCATCCCTA  AGACCCAGT   CCAATACCTG  CTCCCTGAGG  CCAAGGCCCA  300
GGAATCAGAC   AAGATCTGCG  TGGTCATCGA  CCTGGACGAG   ACCCTGGTGC  ACAGCTCCTT  360
CAAGCCAGTG   AACAACGCGG  ACTTCATCAT  CCCTGTGGAG   ATTGATGGGG  TGGTCCACCA  420
GGTCTACGTG   TTGAAGCGTC  CTCACGTGGA  TGAGTTCCTG   CAGCGAATGG  GCGAGCTCTT  480
TGAATGTGTG   CTGTTCACTG  CTAGCCTCGC  CAAGTACGCA   GACCCAGTAG  CTGACCTGCT  540
GGACAAATGG   GGGGCCTTCC  GGGCCCGGCT  GTTTCGAGAG   TCCTGCGTCT  TCCACCGGGG  600
GAACTACGTG   AAGGACCTGA  GCCGGTGGG   TCGAGACCTG  CGGCGGGTGC  TCATCCTGGA  660
CAATTCACCT   GCCTCCTATG  TCTTCCATCC  AGACAATGCT   GTACCGGTGG  CCTCGTGGTT  720
TGACAACATG   AGTGACACAG  AGCTCCACGA  CCTCCTCCCC   TTCTTCGAGC  AACTCAGCCG  780
TGTGGACGAC   GTGTACTCAG  TGCTCAGGCA  GCCACGGCCA   GGGAGCTAGT  GAGGGTGATG  840
GGGCCAGGAC   CTGCCCCCTG  CCAATGATAC  CCACACCTCC   TCCCAGGAAG  ACTGCCCAGG  900
CCTTTGTAG    GAAAACCCAT  GGGCCGCCGC  CACACTCAGT   GCCATGGGGA  AGCGGGCGTC  960
TCCCCACCA    GCCCCACCAG  GCGGTGTAGG  GGCAGCAGGC   TGCAGTGAAG  ACCGTGAGCT  1020
TCAGGCCCCG   TGTCAGTGCC  TTCAAACCTC  CTCCCCTATT   CTCAGGGGAC  CTGGGGGGCC  1080
CTGCCTGCTG   CTCCCCTTTT  CTGTCTCTGT  CATGCTGCC    ATGTTTCTCT  GCTGCCAAAT  1140
TGGGCCCCCT   GGCCCCCTTC  GGTTCGTGCT  CCTGGGGGCA   GGGTTCCTGC  CTTGGACCCC  1200
CAGTCTGGGA   ACGGTGGACA  TCAAGTGCCT  TGCATAGAGC   CCCCTCTTCC  CCGCCCAGCT  1260
TCCCCAGGGG   CACAGCTCTA  GGCTGGGAGG  GGAGAACCAG   CCCCTCCCCC  TGCCCCACCT  1320
CCTCCCTTGG   GACTGAGAGG  GCCCCTACCA  ACCTTTGCCT   CTGCCTTGA   GGGAGGGGAG  1380
GTCTGTACC    ACTGGGGAAG  GCAGCAGGAG  TCTGTCTTTC   AGGCCCCACA  GTGCAGCTTC  1440
TCCAGGGCCG   ACAGCTGAGG  GCTGCTCCCT  GCATCATCCA   AGCAATGACC  TCAGACTTCT  1500
GCCTTAACCA   GCCCCGGGGC  TTGGCTCCCC  CAGCTCTGAG   CGTGGGGGCA  TAGGCAGGAC  1560
CCCCCTTGTG   GTGCCATATA  AATATGTACA  TGTGTATATA   GATTTTTAGG  GGAAGGAGAG  1620
AGGGAAGGGT   CAGGGTAGAG  ACACCCCTCC  CTTGCCCCCT   TCCTGGGGCC  AGAAGTTGGG  1680
GGGAGGGAGG   GAAAGATTTT  TTACATTTTT  TAAACTGCTA   TTTTCTGAAT  GGAACAAGCT  1740
GGGCCAAGGG   GCCCAGGCCC  TGTCTCTGT   CCCTCACACC  CCTTTGCTCC  GTTCATTCAT  1800
TCAAAAAAAC   ATTTCTTGAG  CACCTTCTGT  GCCCAGCATA   TGCTAGGCCC  ACCAGCTAAG  1860
TGTGTGTGGG   GGGTCTCTAC  GCCAGCTCAT  CAGTGCCCTC   TTGCCCATCC  TTCACCGGTG  1920
CCTTTGGGGG   ATCTGTAGGA  GGTGGGACCT  TCTGTGGGGT   TTGGGGATCT  CCAGGAAGCC  1980

CGACCAAGCT   GTCCCCCTTC  CCTGTGCCAA  CCCATCTCCT   ACAGCCCCCT  GCCTGATCCC  2040
CTGCTGGCTG   GGGGCAGCTC  CCAGGATATC  CTGCCTTCCA   ACTGTTTCTG  AAGCCCCCTC  2100
TCCTAACATG   GCGATTCCGG  AGGTCAAGGC  CTTGGGCTCT   CCCAGGGTC   TAACGGTTAA  2160
GGGGACCCAC   ATACCAGTGC  CAAGGGGGAT  GTCAAGTGGT   GATGTCGTTG  TGCTCCCCTC  2220
CCCCAGAGCG   GGTGGGCGGG  GGGTGAATAT  GGTGGCCTG    CATCAGGTGG  CCTTCCCAT  2280
TAAGTGCCTT   CTCTGTGACT  GAGAGCCCTA  GTGTGATGAG   AACTAAAGAG  AAAGCCAGAC  2340
CCCTAAAAAA   AAAAAA      AAAAAA      2369

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(2) INFORMATION ON SEQ ID NO. 224:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 849 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

CGAAACGTGC	GCAGGCGCCG	GCCGCTGCGC	TGCAGATGGC	GGAAATGGAT	CCGGTAGCCG	60
AGTTCCCCCA	GCCTCCCGGT	GCTGCGCGCT	GGGCTGAGGC	CCTTCTGCGA	TGTTTTACCT	120
GGCTGCGGCT	GTGTCAGATT	TCTATGTTCC	TGTCTCTGAA	ATGCCTGAAC	ACAAGATCCA	180
GTCATCTGGG	GGCCCACTGC	AGATAACAAT	GAAGATGGTG	CCAAAACCTGC	TTTCTCCTTT	240
GGTTAAAGAT	TGGGCTCCCA	AAGCATTAT	AATTTCCTTT	AAGTTGGAGA	CTGACCCCGC	300
CATTGTAATT	AATCGAGCTC	GGAAGGCTTT	GGAAATTTAT	CAGCATCAAG	TGGTGGTGGC	360
TAATATCCTT	GAGTCACGAC	AGTCCTTTGT	GTTTATTGTA	ACCAAAGACT	CGGAAACCAA	420
GTTATTGCTA	TCAGAGGAAG	AAATAGAAAA	AGGCGTAGAG	ATAGAAGAGA	AGATAGTGGA	480
TAATCTTCAG	TCTCGACACA	CAGCTTTTAT	AGGTGACAGA	AACTGAAGTA	AAAAGCCCTT	540
ATAGGATCAA	AAATTGTTCA	GGGCTCTTAG	AGATGGTGAA	AACTACAAAA	AAAACCATGG	600
CTTTCATATG	GACAGATAAA	ATGAAAGAGA	GGGAAAAGGC	AGTGGTGTGT	AGGCAAATAT	660
GGTTTGGCAT	TTGTCTTTTA	ATGACACCTG	ATATGATGTC	ATTTTGATTT	TGAAATTGAA	720
CACTAGAACT	GTTAATCACC	TTTAAAAAGG	AAGAGCTTAT	TGGGGATTAT	ATATTCCTTA	780
AAAATATACA	TGGGGGCCTG	AATGTCAGCC	ATCTGTATAC	TGTGGGGAAA	AGGGGTTTGG	840
GTGCAATTC						849

(2) INFORMATION ON SEQ ID NO. 225:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1502 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

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CCTTACCGGC AGGGCTGCCC AGGAGCTGCA GGACAAGCAC CAGGAGCCCC TCCGGGTAGC 60
TACTACCCTG GACTCCCCTC TGGAAGTCCA GGAGGACCAT ATGGCGGTGC AGCTCCCGGG 120
GGCCCCATAG GTCAGCCACC TCCAAGTTCC TACGGTGCCC AGCAGCCTGG GCTTTATGGA 180
CAGGGTGGCG CCCCTCCCAA TGTGGATCCT GAGGCCTACT CCTGGTTCCA CTCGGTGGAC 240
TCAGATCACA GTGGCTATAT CTCCATGAAG GAGCTAAAGC AGGCCCTGGT CAACTGCAAT 300
TGGTCTTCAT TCAATGATGA GACCTGCCTC ATGATGATAA ACATGTTTGA CAAGACCAAG 360
TCAGGCCGCA TCGATGTCTA CGGCTTCTCA GCCCTGTGGA AATTCATCCA GCAGTGGGAAG 420
AACCTCTTCC AGCAGTATGA CCGGGACCGC TCGGGCTCCA TTAGCTACAC AGAGCTGCAG 480
CAAGCTCTGT CCCAAATGGG CTACAACCTG AGCCCCAGT TCACCCAGCT TCTGGTCTCC 540
CGCTACTGCC CACGCTCTGC CAATCCTGCC ATGCAGCTTG ACCGCTTCAT CCAGGTGTGC 600
ACCCAGCTGC AGGTGCTGAC AGAGGCCTTC CGGGAGAAGG ACACAGCTGT ACAAGGCAAC 660
ATCCGGCTCA GCTTCGAGGA CTTCGTCACC ATGACAGCTT CTCGGATGCT ATGACCCAAC 720
CATCTGTGGA GAGTGGAGTG CACCAGGGAC CTTTCTTGGC TTCTTAGAGT GAGAGAAGTA 780
TGTGGACATC TCTTCTTTTC CTGTCCCTCT AGAAGAACAT TCTCCCTTGC TTGATGCAAC 840
ACTGTTCCAA AAGAGGGTGG AGAGTCCTGC ATCATAGCCA CCAAATAGTG AGGACCGGGG 900
CTGAGGCCAC ACAGATAGGG GCCTGATGGA GGAGAGGATA GAAGTTGAAT GTCCTGATGG 960
CCATGAGCAG TTGAGTGGCA CAGCCTGGCA CCAGGAGCAG GTCCTTGTA TGGAGTTAGT1020
GTCCAGTCAG CTGAGCTCCA CCCTGATGCC AGTGGTGAGT GTTCATCGGC CTGTTACCGT1080
TAGTACCTGT GTTCCCTCAC CAGGCCATCC TGTCAAACGA GCCCATTTTC TCCAAAGTGG1140
AATCTGACCA AGCATGAGAG AGATCTGTCT ATGGGACCAG TGGCTTGGAT TCTGCCACAC1200
CCATAAATCC TTGTGTGTTA ACTTCTAGCT GCCTGGGGCT GGCCCTGCTC AGACAAATCT1260
GCTCCCTGGG CATCTTTGGC CAGGCTTCTG CCCTCTGCAG CTGGGACCCC TCACTTGCCT1320
GCCATGCTCT GCTCGGCTTC AGTCTCCAGG AGACAGTGGT CACCTCTCCC TGCCAATACT1380
TTTTTTAATT TGCATTTTTT TTCATTTGGG GCCAAAAGTC CAGTGAAATT GTAAGCTTCA1440
ATAAAAGGAT GAAACTCTGG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA1500
AA

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1502

(2) INFORMATION ON SEQ ID NO. 226:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1892 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

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CATAATTCGC TTTAGAGTCA TTTTCCAGC AATGTTTAAA TTACTTTCTC ATTCTTTTAG 60
TGTATTCAAC ATTGCTCGCC TCTTCCTGCA GTTGATGTAA TTGCTTTGTT TGCAATAGCA 120
CAAGCTGCAT TATTCCAGTC AGGACTGTGA TAACTTGCTG CCAGCCCCAC TCAACTTTCA 180
GTTGGCTCTG TGTCAGTTTT CCCTCAGTG TTACTACTT GTTACTGCCA TGCTGCTTGC 240
CCTCCCTTGA AGTGTCTATA AGCTCATCAG AGCCTAGAGT TAAGTAAAGT CAATTCACAG 300
AAGCACAATT TTGCCCTTTG CGAGACATTG TTGCCTCTAT CTAGTCCTAC AAGTAGGGTT 360
TTGCATACTG TGTTTGCCCC TAGGGTTGTC AGTGCATCAG AAATACTTCT AAATAGTGGT 420
AAAAATGCAC ATGGTTAATG CACATGTTAC TTTTAAATCA TTAGGATATC CCTCACCTGT 480
TCCTGATGAA TAAAAAGTGT GTTAAAGACC AAAATTCTTG GCATAATAAT CAGCTACATA 540
CAAATCACAT ATAGTTTAAAT CTTTTTTAAT GGAAAAAATA TCATGTTTAA AATGGCAAAA 600
GCCCATCTTA TACACTTTTA TATAGCTGCA AAAAATTTAT ATCTGTACAG ATCTAACACT 660
ACGACACTCA GTATTCATTT TATTGAAGCA TGCAAGTAAA GCACTTTTTT TAATTTATAT 720
AGAGGTATCT AATTAACACA GCACATTGTA CTAATGACTA GGAGTAGCAG CTTTTTCTTC 780
TCTCCCTCTA TGAATTCTTA TAATGTCCCT TTTTCTGTAA GTTTTTGAGA GGCAATTGGC 840
AATTTAGGAG GCAGCAGGGT CTGTTTTGGT CAAATCTTGA ATTCGTTGTG TGCACTCTAG 900
TGACTGATCT TTGGGAATGT CTTGTCTTTG CATGGGGCTC ATAGAGATGT GTGCAGACTT 960
GCTTATTGTG GTTAGTGTGT ATCAGGAACA CACACACAGG TGTCTGACC AGCTCAGGCT 1020
TGCCACAGTG AGCAACTCTG TGGCTAGCAA AAGAGAAGTT TATTTGTGCC CAGCCATTGG 1080
TCACCTTGGG TGATGCACCA GATAGCAGGC AGATGTTGGT TCATTGGCCT TCGTCCTCTT 1140
TCCTCTATAA ATAATATTGG CTTTACCATC TTAACCTAGC TGTGGGTTTT TTGTGGGTTT 1200
TTGTTTGTTC TTTGGCATGA ATTGTCATCT TTGGTGTTTT TTTAACCCCC AGCCCCTCAA 1260
AAAAATAAGG CCTCCAGGTA TCAAGATCTC ATATTAGGAT TTTCTGTCCT TAATTTTTTG 1320
AGCAAAATCT GGAAATGTG AAAGCATATT TAGATTTTAT ATACTATCTG AAATGTGATT 1380
TGTTAAGATT CTAAATTTG GGCTCTTAG AATAATTTTG AATGAGATCT ACCGACTCAC 1440
TTGTGAGAAT ATTTTTCACA GATTATCTTT GGGCCTTTTC ATTAGAAAGC TGTTTGTGTT 1500
TCCCCCTGTT GGTACATTTG GTTACCTCAT TTTGCCGTTT CAGATTGTGA AAGCTCACAG 1560
GGGTGTTTTT TGAATCATT TGCTGAGTCA TTTTCTCAA TCATATTCCA TTGTATCAGT 1620
TAACATATAG TTTTAAATGT ATGTATTATA AATATCTGTA ACCAAATCAT TTGAAGGCTT 1680
GATAAATTTT TAACAAAGTT TGTACATTTT TTATGAAAGT TACTAGTAAT GCTTTACTAA 1740
GTAGTGCAAT GAATTTTTAT TTTAATCCC TGTGCCCAAT TTTGGAGTTG AGAGGGTTGT 1800
TGGAATAAAA TGTATGATGT AACTTAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1860
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA

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(2) INFORMATION ON SEQ ID NO. 227:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1522 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

CAGGAGTGCG	GACCAGCGGG	TGCCTGTAGT	GGGTGGAATT	GGGGTCTGCA	CTTGCCCCTC	60
CGCCCCCAGG	TGGGAGTCAC	CTGGAGCGTG	AAGGGACGTG	TCTCATCCCC	AGTGTGTCGG	120
ACCCTGGAGA	CACAGCCGCA	GAGCAGCCCC	TTCTCATGCA	TGGACCTCAC	CTACGTCAGC	180
CTGCTACTCC	AGGAGTTCGG	CTTTCCCAGG	AGCAAAGTGC	TGAAGCTCAC	TCGGAAAATT	240
GACAATGTTG	AGACCAGCTG	GGCTCTGGGG	GCCATTTTTT	ATTACATCGA	CTCCCTGAAC	300
AGACAGAAGA	GTCCAGCCTC	ATAGTGGCCG	AGCCATCCCT	GTCCCCGTCA	GCAGTGTCTG	360
TGTGTCTGCA	TAAACCCTCC	TGTCCTGGAC	GTGACTTCAT	CCTGAGGAGC	CACAGCACAG	420
GCCGTGCTGG	CACTTTCTGC	ACACTGGCTC	TGGGACTTGC	AGAAGGCCTG	GTGCTGCCCT	480
GGCATCAGCC	TCTTCCAGTC	ACATCTGGCC	AGAGGGCTGT	CTGGACCTGG	GCCCTGCTCA	540
ATGCCACCTG	TCTGCCTGGG	CTCCAAGTGG	GCAGGACCAG	GACAGAACCA	CAGGCACACA	600
CTGAGGGGGC	AGTGTGGCTC	CCTGCCTGTC	CCATCCCCAT	GCCCCGTCCG	CGGGGCTGTG	660
GCTGCTGCTG	TGCATGTCCC	TGCGATGGGA	GTCTTGCTCT	CCAGCCTGTC	AGTTTCCTCC	720
CCAGGGCAGA	GCTCCCCTTC	CTGCNAGAGT	CTGGGAGGCG	GTGCAGGCTG	TCCTGGCTGC	780
TCTGGGGAAG	CCGAGGGACA	GCCATAACAC	CCCCGGGACA	GTAGGTCTGG	GCGGCACCAC	840
TGGGAACCTC	GGACTTGAGT	GTGTTTGCCT	CTTCCTTGGG	TATGAATGTG	TGAGTTCACC	900
CAGAGGCCTG	CTCTCCTCAC	ACATTGTGTG	GTTTGGGGTT	AATGATGGAG	GGAGACACCT	960
CCTCATAGAC	GGCAGGTGCC	CACCTTTCAG	GGAGTCTCCC	AGCATGGGCG	GATGCCGGGC	1020
ATGAGCTGCT	GTAAACTATT	TGTGGCTGTG	CTGCTTGAGT	GACGTCTCTG	TCGTGTGGGT	1080
GCCAAGTGCT	TGTGTAGAAA	CTGTGTTCTG	AGCCCCCTTT	TCTGGACACC	AACTGTGTCC	1140
TGTGAATGTA	TCGCTACTGT	GAGCTGTTCC	CGCCTAGCCA	GGGCCATGTC	TTAGGTGCAG	1200
CTGTGCCACG	GGTCAGCTGA	GCCACAGTCC	CAGAACCAAG	CTCTCGGTGT	CTCGGGCCAC	1260
CATCCGCCCA	CCTCGGGCTG	ACCCACCTC	CTCCATGGAC	AGTGTGAGCC	CCGGGCCGTG	1320
CATCCTGCTC	AGTGTGGCGT	CAGTGTCGGG	GCTGAGCCCC	TTGAGCTGCT	TCAGTGAATG	1380
TACAGTGCCC	GGCAGGAGCT	GAACCTCATG	TGTTCCACTC	CCAATAAAAG	GTGACAGGGG	1440
AAAAAAAAAA	AAAAAAAAC	CGAGCGGAAC	GAGCTCACTT	TCTTCTAGCT	GAGCTTTAAA	1500
ACATTAGAGC	TTAAATTTTC	AG				1522

(2) INFORMATION ON SEQ ID NO. 228:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2016 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

GAGAAAATGG	AGGCCTTTGG	GGAAGGGGCA	GGGTGGGAGG	ATTTCTTCTC	CACACAGACC	60
TTAACCTTCC	AATCTATTCT	GCAGATGAAG	AATGCCGACT	ACTTCTCCAA	CTATGTCACA	120
GAGGACTTTA	CCACCTACAT	TAACAGGAAG	CGGAAAAACA	ATTGCCATGG	CAACCACATT	180
GAGATGCAGG	CCATGGCAGA	GATGTACAAC	CGTCCTGTGG	AGGTGTACCA	GTACAGCACA	240
GAACCCATCA	ACACATTCCA	TGGGATACAT	CAAAACGAGG	ACGAACCCAT	TCGTGTTAGC	300
TACCATCGGA	ATATCCACTA	TAATTCAGTG	GTGAATCCTA	ACAAGGCCAC	CATTGGTGTG	360
GGGCTGGGCC	TGCCATCATT	CAAACCAGGG	TTTGAGAGC	AGTCTCTGAT	GAAGAATGCC	420
ATAAAAACAT	CGGAGGAGTC	ATGGATTGAA	CAGCAGATGC	TAGAAGACAA	GAAACGGGCC	480
ACAGACTGGG	AGGCCACAAA	TGAAGCCATC	GAGGAGCAGG	TGGCTCGGGA	ATCCTACCTG	540
CAGTGGTTGC	GGGATCAGGA	GAAACAGGCT	CGCCAGGTCC	GAGGCCCCAG	CCAGCCCCGG	600
AAAGCCAGCG	CCACATGCAG	TTCGGCCACA	GCAGCAGCCT	CCAGTGGCCT	GGAGGAGTGG	660
ACTAGCCGGT	CCCCGCGGCA	GGGAGTTCAG	CCTCGTCACC	TGAGCACCCCT	GAGCTGCATG	720
CTGAATTGGG	CATGAAGCCC	CCTTCCCCAG	GCACGTGTTT	AGCTCTTGCC	AAACCTCCTT	780
CGCCCTGTGC	GCCAGGTACA	AGCAGTCAGT	TCTCGGCAGG	GGCCGACCGG	GCAACTTCCC	840
CCCTTGTGTC	CCTCTACCCT	GCTTTGGAGT	GCCGGGCCCT	CATTCAGCAG	ATGTCCCCCT	900
CTGCCTTTGG	TCTGAATGAC	TGGGATGATG	ATGAGATCCT	AGCTTCGGTG	CTGGCAGTGT	960
CCCAACAGGA	ATACCTAGAC	AGTATGAAGA	AAAACAAAGT	GCACAGAGAC	CCGCCCCCAG	1020
ACAAGAGTTG	ATGGAGACCC	AGGGATTGGA	CACCATCTCC	CAACCCCAGT	ACTCCTGCTC	1080
TCCGGTGCCA	CCTCACCTTC	TTTGGCTTCT	TCCCTCTTGC	CTCCTTCTGT	TCTTTCTGCT	1140
CTCCCCTCTT	TTCCCTCCTC	CTCACTTCCC	TCTGGCTAGC	CCACCCCTGC	ACTCTCTCTC	1200
ATTGCCGCTG	CCACTATCAC	CTGTCTCTCT	GCCAGCTGAT	GTGCCCTGTT	GCCCCCACC	1260
CCATCCCGCA	CAGAACCATC	CCTGCATTCC	ACAGGGGACT	CGGGCAAGGG	TGCCGAAGAT	1320
AGACAAGAGG	CACACAGAGA	CAGACCAACT	GGCAGCCAGG	CAGCCCCAGA	GGAGAGAGAC	1380
ATTGAGACAG	AGGAAAGTCT	CCCTGCCCTT	CATTCCTTCC	AAGATGAGAA	AAACTTGCCG	1440
CCACCCCCCG	ACACTGATGC	CAGGGAGGTG	GGAGGAAGAA	GTGGGAAATT	TCCCTTCCCA	1500
GTACCCCCAA	GAACGTCTGA	GCCTTCAATG	TTGAATTTT	TCTTTATTAA	AATTACTTTT	1560
ATCTTATAAA	ATCAACTAAT	CAAAAATGAT	ATAGACGACA	GCACTGGCTC	TGTGAAGGTG	1620
GCATCTTTCT	GGGCAGGCAG	GCCATGGGGC	ATGGAGGAGG	GTGCAAAGAT	ATGGGTGTGC	1680
GTCTTCTGGC	CTCCAGCTGC	ATGGAGGCCG	GCCCAGGGTC	TAGGGTGTGC	ACTGGGCAAG	1740
GGCAGGGCGG	CAGGTGTCAG	GCCGGCTTGG	ACAATGAAAC	CCTGACCTTG	CTGCATTCTT	1800
TTTGCTTCCA	CCACCACTAG	CTTCTTTGGA	ATCTTGGGGT	GGGGGTCATC	TTTGGGGATT	1860
ATGGCTGCCA	CCCGGGATTT	GAGTGTAGGG	AGTGTGGGAG	CAGCCTTGCC	AGAAGGGGCA	1920
CCCGTGCCCT	GCAGGTGTTG	ACAAGATCCG	CCATCTGTAA	TGTCCTTGCC	ACAATAAAAC	1980
CAAATGTCAG	TTTCAAAAAA	AAAAAAAAAA	AAAGAC			2016

(2) INFORMATION ON SEQ ID NO. 229:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 765 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

CCGGATTCCG	CCCCGCCCCG	TGCGATCCGG	TTCCGCTCCC	CACAACCCGC	TCTGTGGCGG	60
GGCTTCCGGT	CGGGAGGGTC	CGCCAGCTCT	CGCGTCCTTT	GCTGGGTCCA	GACACCGGTT	120
CCGTTGCAA	CATTTTAAA	GGGCTGGTTA	TTCTTCCTGA	AATGAGTTTG	GTGATTAGAA	180
ATCTGCAGCG	AGTCATCCCC	ATCAGGAGAG	CGCCACTTCG	CAGTAAGATC	GAGATTGTAA	240
GGAGGATTTT	AGGAGTGCAG	AAATTTGACC	TGGGGATCAT	CTGTGTTGAC	AACAAGAATA	300
TTCAGCACAT	TAATAGAATC	TACAGAGATA	GAAATGTCCC	AACCGATGTG	CTTCTTTTTC	360
CATTTTCATGA	GCATCTGAAA	GCAGGTGAAT	TTCCCCAGCC	TGATTTTCCA	GATGACTACA	420
ATTTGGGAGA	CATTTTCCTA	GGAGTGGAGT	ATATCTTCCA	TCAGTGTAAG	GAAAATGAAG	480
ATTACAATGA	CGTCCTGACT	GTGACGGCCA	CCCACGGACT	CTGTCACTTG	CTGGGATTCA	540
CACACGGCAC	GGAGGCAGAG	TGGCAGCAGA	TGTTCCAGAA	GGAGAAGGCG	GTGCTGGACG	600
AGCTGGGCGG	ACGCACGGGG	ACCCGGCTGC	AAGCCCTGAC	CCGGGGCCTC	FTCGGAGGGA	660
GCTGAGGGCC	GCGTTCCTTC	TGAAAGCGGG	ACGCGGGAGG	GGTGGAGGCT	GCGGGGAGCC	720
GGGGTCGCAC	ACAAATAAAT	AACGAATGAA	CGTAAAAAAA	AAAAA		765

(2) INFORMATION ON SEQ ID NO. 230:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1611 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CTGCTTGGCG CGACGCTCTA GCGGTTACCG CTGCGGGCTG GCTGGACCGT AGTGGGGCTG 60
CGCGGCTGCC ACGGAGCTAG AGGGGTTAAA AACTAATATT TATATGACAG AAGAAAAAGA 120
TGTCATTCCG TAAAGTAAAC ATCATCATCT TGGTCCTGGC TGTGCTCTC TTCTTACTGG 180
TTTTGCACCA TAACTTCCTC AGCTTGAGCA GTTTGTAAAG GAATGAGGTT ACAGATTGAG 240
GAATTGTAGG GCCTCAACCT ATAGACTTTG TCCCAAATGC TCTCCGACAT GCAGTAGATG 300
GGAGACAAGA GGAGATTCCCT GTGGTCATCG CTGCATCTGA AGACAGGCTT GGGGGGGCCA 360
TTGCAGCTAT AAACAGCATT CAGCACAACA CTCGCTCCAA TGTGATTTTC TACATTGTTA 420
CTCTCAACAA TACAGCAGAC CATCTCCGGT CCTGGCTCAA CAGTGATTCC CTGAAAAGCA 480
TCAGATACAA AATTGTCAAT TTTGACCCTA AACTTTTGGA AGGAAAAGTA AAGGAGGATC 540
CTGACCAGGG GGAATCCATG AAACCTTTAA CCTTTGCAAG GTTCTACTTG CCAATTCTGG 600
TTCCAGCGC AAAGAAGGCC ATATACATGG ATGATGATGT AATTGTGCAA GGTGATATTC 660
TTGCCCTTTA CAATACAGCA CTGAAGCCAG GACATGCAGC TGCATTTTCA GAAGATTGTG 720
ATTCAGCCTC TACTAAAGTT GTCATCCGTG GAGCAGGAAA CCAGTACAAT TACATTGGCT 780
ATCTTGACTA TAAAAAGGAA AGAATTCGTA AGCTTTCCAT GAAAGCCAGC ACTTGCTCAT 840
TTAATCCTGG AGTTTTTGTG GCAAACCTGA CGGAATGGAA ACGACAGAAT ATAATAACC 900
AACTGGAAAA ATGGATGAAA CTCAATGTAG AAGAGGGACT GTATAGCAGA ACCCTGGCTG 960
GTAGCATCAC AACACCTCCT CTGCTTATCG TATTTTATCA ACAGCACTCT ACCATCGATC 1020
CTATGTGGAA TGTCGCCAC CTTGGTTCCA GTGCTGGAAA ACGATATTCA CCTCAGTTTG 1080
TAAAGGCTGC CAAGTTACTC CATTGGAATG GACATTTGAA GCCATGGGGA AGGACTGCTT 1140
CATATACTGA TGTTTGGGAA AAATGGTATA TTCCAGACCC AACAGGCAA TTCAACCTAA 1200
TCCGAAGATA TACCGAGATC TCAAACATAA AGTGAAACAG AATTGAACT GTAAGCAAGC 1260
ATTTCTCAGG AAGTCCTGGA AGATAGCATG CGTGGGAAGT AACAGTTGCT AGGCTTCAAT 1320
GCCTATCGGT AGCAAGCCAT GGAAAAAGAT GTGTCAGCTA GGTAAAGATG ACAAAGTCC 1380
CTGTCTGGCA GTCAGCTTCC CAGACAGACT ATAGACTATA AATATGTCTC CATCTGCCTT 1440
ACCAAGTGTT TTCTTACTAC AATGCTGAAT GACTGGAAAG AAGAACTGAT ATGGCTAGTT 1500
CAGCTAGCTG GTACAGATAA TTCAAACTG CTGTTGGTTT TAATTTTGTA ACCTGTGGCC 1560
TGATCTGTAA ATAAACTTA CATTTTTC AAATAAAGA T 1611

(2) INFORMATION ON SEQ ID NO. 231:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1473 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

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GGTGTGGTCC TCAGGGGGCT GTAGGGTGGG AGGTATGGCT TCAGGTGCCA AGTTGGCGGG 60
AACGGCAGCG AGGAGGCCTG GGGGGCACTT CGGGCGCCGC AACAGCAGGT ATCCCAATAG 120
CTCCAAAACC TATCACGACA GCCATTTGTC TCTTTCCCCT TTCCTTGTCC CTTCTTTTG 180
GGGGTGGGGG AGGAACTCAC GGAGCCAAAG GTACTGTGAA GTTCCTAAAC ATGTCTCTTC 240
CACTCTTTGT CTAAACTTTG TAACGTAGAT GCAGCTGACT TTGCCTGTAG CCTCATAGAA 300
CCCATCCCAT GGCTGCAGTG GAAGCTTGCG GTGGCTCTCC AGTGACCAGA GGCATAGTGA 360
GGTCCCAGGG AGGCTCCCTC TGTCTTGCAA CAGTTATTTG TGATCTTTTT CTATGTGCCT 420
ATTGTCACAA CAGAGTCCGG CAGCGTCTTC TCTTGAGGGA GCAATTTGGA GAAGAGCTGG 480
AACCCAGACT CGCGCCCTGG ATGCCATCCT TTATCATCCA CAGCAATCCC ATCTGGTTGG 540
GAGCACTGCT CTGGGTCTCA CACTGCCCTT CCTCTATCCT AGGGAGCCTG AGGCCCAGGG 600
GTGGAAAGAT CCAGTTGCGG GTGGGGGGTA GTGAACCGTG CAGGATAATG AAAGCAACTT 660
GCTTTGGAAT TGACCTACCG CTACCCGTTG TCTGAGACTG AGATTATCTC AGACTGTCTT 720
CTGGCTTCTG CCAAACACT CCCTTAACAG AAAGCACCGA GGGGATGGGG GTAGGGGGGT 780
TGGGGAGAGT GAGGCTTGAG TGTGAAGGAA GTCTCATATA TGCAGAGCTG AAATCTCCCT 840
CTTTGTATGT CCACACTTTT GTCTTGTCTT CTAGACTGAT TCTTGCTATT CCAAATCCTC 900
TTCCACGTTG ACAGCCCTTC AGATATTTCA ACACTCCTCT CAGCATCCTC CACTTCCCCC 960
ATCTCTCCAA GCTGAACTTG GTTACACAGG TGGGATTGTG TATGTGCATG CAGGAGGTGG1020
GGGTGGACAG TGCCCTGGGC TGGAATCCCC CTTAGTTCTA AGTGCCTCCT TGCCCGCAGC1080
TTCGAGAGCT GTGCCAGGA GTGAACAACC AGCCCTACCT CTGTGAGAGT GGTCACGTCT1140
GCGGGGAGAC TGGCTGCTGC ACCTACTACT ATGAGCTCTG GTGGTTCTGG CTGCTCTGGA1200
CTGTCCTCAT CCTCTTTAGC TGCTGTTGCG CCTTCCGCCA CCGACGAGCT AAACCTCAGGC1260
TGCAACAACA GCAGCGGCAG GTGGAAATCA ACTTGTGGG CTATCATGGG GCATGCCATG1320
GGGCTGGTCC TTTCCCTACC GGTTCACCTG TTAGCTTTCG CTTCTCAGC ACCTTCAAGC1380
CCCCAGCCTA CGAGGATGTG GTTACCGGCC CAGGCACAAC GAGCCCCCCC TTATACTGTG1440
GCCCCAAGGC GCCCCTTGAG GTTGTTCCTA GTG

```

(2) INFORMATION ON SEQ ID NO. 232:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2503 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

GAAACATGCA	ACTGAACAGG	AAAAAACTGA	AGAGGGATTA	GGCCCTAATG	TAAAAGGCAT	60
TGTCACCATG	TTGATGCTGA	TGCTATTGAT	GATGTTTGCG	GTCCACTGTA	CCTGGGTCAC	120
AAGCAATGCC	TACTCTAGTC	CAAGTGTAGT	CCTGGCCTCA	TACAATCATG	ATGGCACCAG	180
GAATATCTTA	GATGATTTTA	GAGAAGCTTA	CTTTTGGCTA	AGGCAAAATA	CAGATGAACA	240
TGCACGAGTA	ATGTCTTGGT	GGGATTATGG	CTATCAGATA	GCTGGAATGG	CTAATAGAAC	300
TACGTTGGTG	GATAATAACA	CCTGGAATAA	CAGCCACATA	GCACTGGTGG	GAAAAGCTAT	360
GTCTTCTAAT	GAAACAGCAG	CCTATAAAAT	CATGAGGACT	CTAGATGTAG	ATTATGTTTT	420
GGTTATTTTT	GGAGGGGTTA	TTGGCTATTC	TGGTGATGAT	ATCAACAAAT	TTCTCTGGAT	480
GGTTAGGATA	GCTGAAGGAG	AACATCCCAA	AGACATTCGG	GAAAGTGAAT	ATTTTACCCC	540
ACAGGGAGAA	TTCCGTGTAG	ACAAAGCAGG	ATCCCCTACT	TTGTTGAATT	GCCTTATGTA	600
TAAAATGTCA	TACTACAGAT	TTGGAGAAAT	GCAGCTGGAT	TTTCGTACAC	CCCCAGGTTT	660
TGACCGAACA	CGTAATGCTG	AGATTGGAAA	TAAGGACATT	AAATTCAAAC	ATTTGGAAGA	720
AGCCTTTACA	TCAGAACACT	GGCTTGTTAG	GATATATAAA	GTAAAAGCAC	CTGATAACAG	780
GGAGACATTA	GATCACAAAC	CTCGAGTCAC	CAACATTTTC	CCAAAACAGA	AGTATTTGTC	840
AAAGAAGACT	ACCAAAAGGA	AGCGTGGCTA	CATTAAAAAT	AAGCTGGTTT	TTAAGAAAGG	900
CAAGAAAATA	TCTAAGAAGA	CTGTTTAAAT	GCACTGTTCT	GGTTCCTAAC	TTGAAGCAGT	960
TGTCCTTGTG	AGAACCGGTC	TTTGCCTTTA	GCTCATGTCG	TGTTTCACAG	CAAAGAGGGT	1020
ACAGAACCAT	CACTGGTCCA	GGTTAATGTA	CAAAATTTTC	TGGCAATGCC	TGATTAAAAA	1080
AATAAAATTG	GCTTGTTGAG	AACAGCTGTT	TTTCGATTCT	AATGTGAAGC	AAGACAGAGC	1140
ACTGCTGTAA	ATGTCTAGCA	GCAGATTTTT	TTTTTATTGG	TACATATTAT	CCTTCAAATC	1200
TGAGAATTTG	GACTAACTGC	ACCAAAGAAC	CCTCTAATTT	GGTCCCTGGC	ACATGCATAC	1260
TTGTCAATGT	TTTTATTCTT	TTACAAGACC	TGCATTTTAT	TTGAATTACC	CGAATAGCAA	1320
TATGTAAAAT	ACAAGTGACA	AAATGTGATG	AGAGCTTCTT	GAACCGGTAA	ACTAGTACAG	1380
GTCTGAGAAA	GACATATTAG	AAGAATCATT	ATACTTCCTT	GAATTATATT	TATTTTCATG	1440
TTTCTCTAAT	GCAAAGAATG	TTTCATCAAA	TGTATATTTT	CTGTTGCTTA	CTGTTTGCTC	1500
TGAGAAGAAG	CTGCTGTTTC	AAAGATGGAC	CTCTGAGTAG	CTAATTGATT	CAAGTAGTTT	1560
TTTTATGTTG	ACACATTATT	ACTGCTGTTA	GCAGTCGTTT	TCACCAGGTA	CTTACAGAGC	1620
AGATTTTCATA	CATCATTCAT	TCAAGGGCTA	AATTTATATT	TTTTGGAAAT	CATGGCAACT	1680
ACACAGGATG	TTGCTTACCA	GGACGGAGTT	TTGGTATCTT	AGTACTGAAG	TTAGCACTAT	1740
GTTTACATGC	AAAAGATTAA	GGAAAAAACC	CTTAAAGTGG	ACAGGTATCC	AAAGTTCATT	1800
TTCTGTGACT	CATCAAAGTG	ACAAAAGACT	TGTAACAAC	TTGCCTGGAC	TTTTTTTCATT	1860
TTACAACAGT	TCATCCATTC	ACAATGATTT	TGTTCTCTGC	TCCATATTTT	TTAATCCCTT	1920

AAGCATTTGA TGAAACACTC TTAGTGCTA TATGCATTTT CTTACTTTTG TTAAAAATGT1980
 GACAATTGTC AAAAAATGCA CTAAAATGTA AATGGAGATT GAACAAGTTC ACTTTCCAGC2040
 TTATAGGCAA CTTTATACAG ACTTGAACAT TTTCTCCAGT TGTTTAGTAA AAGTGAAAGA2100
 GAAAGGGTTT TTCCTGCCAC AGGATATAAC TTTTTTTTAT ATAACAAGCA TAACACACCA2160
 CTGCTTTTGG TGGAAAAGTG CAGAATAGTA TGTACCTTTT ATGAAGAAAA ATGTAATTTA2220
 CAATATTCAG TGAGAATGTT ACTGCTGATT TTCTTTTCCA AGGTGTAGAA TATTCTTTGA2280
 TTTATAGAAT TCATTTTTGA CCCAGATGAT GGTTCTTTTA CAGAACAATA AAATGGCTGA2340
 ACATTTTCAC AAATAGAGTG TAACGAAGTC TGGATTCTG ATACCTTGTC ATTTGGGGGA2400

TTTTATTTTA CTTTGTTGCT TTAAAATTCA ATGCAGAGAA GTTGTTGACT GTAGGGGAAA2460
 TAAAGTTAAT TCAAATTTTG AAAAAAAGTCG ACG 2503

(2) INFORMATION ON SEQ ID NO. 233:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1756 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

AAGCAACCTC GTTTATGTCT TATCTTTGCA TTTTCCTGTA TTCAGCTATT TTCTTAAAGG 60
 AAGGCCCAGG TCTGTATTAT CCTACTGCCA CATAGGAAGT AAAATGAGTA CTCACAGCCT 120
 TGCGCCTAAT CACTGAACAC AGCTTTTAGT AATGTTTTAC ACAAGAACAG GATATTGGCA 180
 ACTCAACTGT TAAGCCTTTC TGTGATTATT CTTCCCTGAG ATCACTCTGA TGTCACCACT 240
 GTAATTTGAG CCTGGAGCTT TTGTTACAC TTTAAATAGC AGTCCCAGAA TGATTTCACT 300
 ACAGACTCTC TGGAAAGCCT GGGAGCTGAA TTCCGGAAGA TCCCACATC GATGAAAGCA 360
 AAGCGAAGCA CCAAGCCATC ATCATGTCCA CGTCGCTACG AGTCAGCCCA TCCATCCATG 420
 GCTACCACTT CGACACAGCC TCTCGTAAGA AAGCCGTGGG CAACATCTTT GAAAACACAG 480
 ACCAAGAATC ACTAGAAAGG CTCTTCAGAA ACTCTGGAGA CAAGAAAGCA GAGGAGAGAG 540
 CCAAGATCAT TTTTGCCATA GATCAAGATG TGGAGGAGAA AACGCGTGCC CTGATGGCCT 600
 TGAAGAAGAG GACAAAAGAC AAGCTTTTCC AGTTTCTGAA ACTGCGGAAA TATTCCATCA 660
 AAGTTCAGTG AAGAGAAGAG GATGGATAAG GACGTTATCC AAGAATGGAC ATTCAAAGAC 720
 CAAGTGAGTT TGTGAGATTG TAACAGATGC AGCATTTTGC TGCTACCTTA CAAGCTTCTC 780
 TTCTGTCAGG ACTCCAGAGG CTGGAAAGGG ACCGGGACTG GAAAGGGACC AGGACTGAAC 840
 AGACTGGTTA CAAAGACTCC AAACAATTC ATGCCCTGTG CTGTTACAGA GGAGAACAAA 900
 ATGCTTTCAG CAAGGATTTG AAAACTCTT CAGTCCCTGCA GGAAAGGATT GATGCTGATA 960
 GAAGAGCCTG GACAGATGTA ATGAGAACTA AAGAAAACAG ATGGCTGGAG ATGACATTTA1020
 TCCAGGGTCA CTTTGTGAGG CCCTAGGACT TAAATCGAAG TTGAACTTTT TTTTTTTTTT1080

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AACCAAATAG ATAGGGGAGG GGAGGAGGGA GAGGGAGGAC AGGGAGAGAA AATACCATGC1140
ATAAATTGTT TACTGAATTT TTATATCTGA GTGTTCAAAA TATTTCCAAG CCTGAGTATT1200
GTCTATTGGT ATAGATTTTT AGAAATCAAT AATTGATTAT TTATTTGCAC TTATTACAAT1260
GCCTGAAAAA GTGCACCACA TGGATGTTAA GTAGAAATTC AAGAAAGTAA GATGTCTTCA1320
GCAACTCAGT AAAACCTTAC GCCACCTTTT GGTTTGTAAA AGGTTTTTTA TACATTTCAA1380
ACAGGTTGCA CAAAAGTTAA AATAATGGGG TCTTTTATAA ATCCAAAGTA CTGTGAAAAC1440
ATTTTACATA TTTTTTAAAT CTTCTGACTA ATGCTAAAAC GTAATCTAAT TAAATTTTCAT1500

ACAGTTACTG CAGTAAGCAT TAGGAAGTGA ATATGATATA CAAAATAGTT TATAAAGACT1560
CTATAGTTTC TATAATTTAT TTTACTGGCA AATGTCATGC AACAATAATA AATTATTGTA1620
AACTTTGTGA AAAATAGTCT GTGATGCTTG GTCTCAAAGG AAAAAATAAG ATGGTAAATG1680
TTGATATTTA CAAACTTTTC TAAAGATGTG TCTCTAACAA TAAAAGTTAA TTTTAGAGTA1740
AAAAAACGG CTCGAG 1756

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(2) INFORMATION ON SEQ ID NO. 234:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1286 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

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GCCTAGGATC CCTGTGACCC TCAACATGAA GATGGTGATG CCCTCCTGTC AAGGCCTTGA 60
TTGAGCATGA AATGAAGAAC GGGATCCCTG CCAATCGAAT CGTCCTGGGA GGCTTTTCAC 120
AGGGCGGGGC CCTGTCCCTC TACACGGCCC TCACCTGCCC CCACCCTCTG GCTGGCATCG 180
TGGCGTTGAG CTGCTGGCTG CCTCTGCACC GGGCCTTCCC CCAGGCAGCT AATGGCAGTG 240
CCAAGGACCT GGCCATACTC CAGTGCCATG GGGAGCTGGA CCCCATGGTG CCCGTACGGT 300
TTGGGGCCCT GACGGCTGAG AAGCTCCGGT CTGTTGTAC ACCTGCCAGG GTCCAGTTCA 360
AGACATACCC GGGTGTCATG CACAGCTCCT GTCCTCAGGA GATGGCAGCT GTGAAGGAAT 420
TTCTTGAGAA GCTGCTGCCT CCTGTCTAAC TAGTCGCTGG CCCCAGTGCA GTACCCCAGC 480
TCATGGGGGA CTCAGCAAGC AAGCGTGGCA CCATCTTGGA TCTGAGCCGG TCGAGCCCT 540
GTCCCCACCC TTCCTGACCT GTCCTTTTCC CACAGGCCTC TGGGGGCAGG TGGCAAGGCC 600
TGGCCGGGCC TTCCTTCCCTG GCCTTAGCCA CCTGGCTCTG TCTGCAGCAG GGGCAGGCTG 660
CTTTCTTATC CATTTCCCTG GAGGCGGGCC CCCCTGGCAG CAGTATTGGA GGGGCTACAG 720
GCAGCTGGAG AAAGGGGCCC AGCCGCTGAC CCCTCACTC AGGACCTCAC TCACTAGCCC 780
CGCTTTGGGC CCCCTCCTGT GACCTCAGGG TTTGGCCCAT GGGGCCCTCC CAGGCCCTG 840
CCCCAACTGA TTCTGCCCAG ATAATCGTGT CTCCTGCCTC CACTCAGCTG CTTCTCAGTC 900
ATGAATGTGG CCATGGCCCC GGGGTCCCCT TGCTGCTGTG GGCTCCCTGT CCCTGGGCAG 960
GAGTGCTGGT GAGGAGGTGG AGCCTTTTGA GGGGGGCCTT CCCTCAGCTG TTTCCCCACA1020
CTGGGGGGCT GGGCCCTGCC TCCCCGTTAC CCTCCTTCCC TGCAGGCCTG GAGCCTGTAG1080
GGCTGGACTG AGGTTTCAGG CTCCCCCAG CTGTCTCACC CCCACTTTGT CCCCCTCTA1140
GAGCAGGGAG GCAAGTGGGG AGGAGTTGTG TCTCGTCTTC TGTCTCCATG TGGTTTTTGG1200
GTGTTTTTCT TGTGTGTCC TGGATTCCGA TAAATTTAA GAAATTGCTT CCTCAAAAAA1260
AAAAAAAAA AAAAAAAGT CGACGC

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(2) INFORMATION ON SEQ ID NO. 235:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

ATTCGGCAAC GAGGTGAGAA AATCCCTTTT AAGGCCAAGG AAAGCTGAAT GCTAGCAGCC 60
 AGGCCTGTGG TACTTCCATG AGAAACCATA GCAGACAATG CCCTCCCAAG TACTGAAATC 120
 ACACTGGAAT CCCCTTTGTT GGGTTCATTT GATTGTTTAA CACAGGATGT GTTGTGTCAT 180
 TCTGAAGTTT TTATTTGGGG CAGAAGTCTT TATGGAGATG TAAATGACAG CGTTTCTGGG 240
 TTATGCATAA CTTCTCACTG GTCAGAGACA CCGGTGTGTC AAGCATGGAT ATTGCATTGC 300
 AAGACTTGAA TCTATAAAAA TTAGAATCAC ACAGTCAGTA CTACAAGCAA AACAGAGAAC 360
 CTGAAAGAAG GTGCACAGAC TGTAAGAAAA AACCCAAGTT TGTGATATTT CAGTGATTCC 420
 AAAGAACATT CTAGGTTTTT TGTGTTTTT TTTGTTTTTT GGGTTTTTTT TTTTACTGCA 480
 GAAAATTGGT GGTATTTTCA CATTCAAGT GTTTCTATCC AATTTCAGTA CCCACATTTA 540
 ATGAGGAAAA AATGTTTTAC CAATGAAGGA GGAATTCTTA AATTAGCTGT AATGTTAGGT 600
 TGGAGAAAAT TTGGTATTTA GGGTATTTTC AAGGTACCAT CAAATCAGAT TTCTGTTTTT 660
 TTGTTAAAAA AAATTTTTTT AATCAGTATT GTTTTTTACAA GTAATATACT TTGAAACTCT 720
 TGAATAATA GTCTCAAAAA CTCTAGAGGA CAGTCTGAGA ACACGTATTT CTATTGTTCT 780
 AAATAAATAC ATGTTTTTGA ATAGTTCAAT CATGAATTAT TGACTATGTC TTCATCAAAA 840
 GTGTTAATCC CTCTCAGGGT CTCTGGTGAA GACCTTCAAG AGTTTGGTTT TTTCTCCCAG 900
 GAAATTGGAA GGTAGAATTG TAAATTCATA GAACTTCTTT TATAATGGTG TACCTCAGCA 960
 GCTGCCTTTC AATTTATGCC AAGTCCTTAC AGAGTTTATA CTTGAATAGT AAATATGTCT 1020
 TCTGAGTTTT ACAGTGCTTT AAACCAATG CACATTTTTT TTTCTTCTTT TTCCACCCCT 1080
 TCTTGTTTGT AGTTCATTAT ACCTGTCCTA TTACAGAACT GATTTCCTTC CTGGCTGTAC 1140
 ATGTTGGGGT GCTGGATTTT TTTCCGTGTC TTTAGTCTTC GGATACATGT TCTCTTCTTT 1200
 AGCTTGTGGT GAATACAGTA ATTTGCATTG 1230

(2) INFORMATION ON SEQ ID NO. 236:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2328 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

U0123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

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TGAGAGTTTA GTTGTAGCAG AGGGGCCACA GACAGAAGCT GTGGTGTTT TTA CTTTGTG 60
CAAAAAGGCA GTGAGTTTCG TGAAGCCTGG AAGTTGGCCA TGTGTCTTAA GAGTGGCTGG 120
ACTTTGACAT GTGGCTGTTT GAATAAGAGA AGGACAAAGG GAGGAGAAAG CACATGTGCT 180
CCAGTGAGTC TTCGTCACTC TGTCTGCCAA GCAATTGATA TATAACCGTG ATTGTGTCTC 240
TGCTTTTCTT CTGAAATGTA GATAACTGCT TTTTGACAAA GAGAGCCTTC CCTCTCCCCC 300
ACCCCTGTGT TCTTGGGTAG GAATGGGAAA AGGGGCAACC TACAAAGATT GTTGGGGCAA 360
GGGAAGTCAC AAGCTTTCGG ATGGGCGGTG GCTTTTCACA AAACATTTAG CTCATCTTAT 420
TCTCTCTTTG TCCTCTCTCC CCTCCTGCCC GCCCGCACCC TGGGAATTGCC ACTCAGTTCC 480
TCTGGGTGTG CACATATGTT TGGAGAAATA GAGGAGAGAA AAGAGGGCCA CGTAACTGAG 540
AGCTTACAGT GCCAATGCCG TTTGTGTTCT GGCCAGAGTG GAGTGCGCAG CCTGACTCCC 600
AGGCGCTGAG ATTGTTGCCT GGTTACCCAG GAAGCTGCTG TTCCGGCTGC CCAGCCTTTC 660
TCTGAGCCAG CGGATGCACA GTCCGTGGCC TTCTTCAGGC TTATTGATGA TGCTTTTGTG 720
AAATGTTGAA TCATGGTTCT GTTCTAAGT TGGATCTTTT TTGTTTTCTC CTGCCCACCC 780
TAATTTGACA TCAAAATTCT CTCTTGTCAG TTGGGCCCTG GGTCAATTCAA ACCCAGGTCA 840
CCTCATTCCC CTTCTCTGTT CACACCTAAT GTCTTGAAGA GTAGGTAGCA GCAGTGTGGG 900
CTGAACCTAG GCCAGCTTGC TTAGCGGGTC ACCCTGCTGT GAAGTCCTGG CAGGTGTTGG 960
TAATGTGTGG AAATGCAGTC AGCAAGTTTG CTGGGGAGTT TGATAAAAGT ATAAAACAAA1020
ACAAAAAAG CCTCGGTATA ATTTTGTTC ACGACTTCTT CTGTAGCTTT ACACCAGAAG1080
GAAGGAATGG GCTACAGCAG GTAGTGAGG AAGAGGGGGG TGAGCAGGTG TATTAAAATA1140
GCTTACGGGT AAGGCCTAAA AGGTCACCCC TCGGCCCCCT CTCCAAAAGA AGGGCATGGG1200
CACCCCCAGG AGAGGATGGC CCAAAAACC TTATTTTAT ACATGAGAGT AAATAAACAT1260
ATTTTTTTTA CAAAAATAAC TTCTGAATTT ATCAGTGTTT TGCCGTTAAA AATATTCCTC1320
TATAGTAAAT TATTTATTGG AAGATGACTT TTTTAAAGCT GCCGTTTGCC TTGGCTTGTT1380
TTCATACACT GATTTATTTT TCTATGCCAG GCAGTAGAGT CTCTCTGCC CTGAGGAGCA1440
GGCTACCCGC ATCCCACTCA GCCCCTCCCT ACCCCTCAAG ATTTGATGAA AATTCCAACC1500
ATGAGGATGG GTGCATCGGG GAAGGGTGAG AAGGAGAGCC TGCCTGCTCA GGGATCCAGG1560
CTCGTAGAGT CACTCCCTGC CCGTCTCCCA GAGATGCTTC ACCAGCACCT GCCTCTGAGA1620
CCTCGCTCTC TGTTCAGCA ACCCTGGTTG GGGGGTCAGA CTTGATACAC TTTAGGTTG1680
GGAGTGGACC CACCCAGGG CCTGCTGAGG ACAGAGCAGC CAGGCCGTCC TGGCTCACTT1740
TGCAGTTGGC ACTGGGTTGG GGAGGAAGAG AGCTGATGAG TGTGGCTTCC CTGAGCTGGG1800
GTTTCCCTGC TTGTCCAGTT GTGAGCTGTC CTCGGTGTTA CCGAGGCTGT GCCTAGAGAG1860
TGGAGATTTT TGATGAAAGG TGTGCTCGCT CTCTGCGTTC TATCTTCTCT CTCCTCCTTG1920
TTCCTGCAAA CCACAAGATA AAGGTAGTGG TGTGTCTCGA CCCCATCAGC CTCTCACCCA1980

CTCCCAGACA CACACAAGTC CTCAAAAGTT TCAGCTCCGT GTGTGAGATG TGCAGGTTTT2040
TTCTAGGGGG TAGGGGGAGA CTAATAATCGA ATATAACTTA AAATGAAAGT ATACTTTTTA2100
TAATTTTTCT TTTTAAACT TGGTGAAATT ATTTAGATA CATATTTTAG TGTCAAGGCA2160
GATTAGTTAT TTAGCCACCA AAAAAAAGTA TTGTGTACAA TTTGGGGCCT CAAATTTGAC2220
TCTGCCTCAA AAAAAAGAAA TATATCCTAT GCAGAGTTAC AGTCACAAAG TTGTGTATTT2280
TATGTTACAA TAAAGCCTTC CTCTGAAGGG AAAAAAAAAA AAAAAAAA 2328

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(2) INFORMATION ON SEQ ID NO. 237:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1767 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

TGTGACATTG TCCTGAGGTT CATCCGCCTA AATTATTATT AGCCATCCCT TACCAAATAT 60
 TTCAAACCAG GCAAATGACT TCTGGAAGAG AGAGAAAGGA AGGGGAGAGG GAGGGAGAAT 120
 GTGAGTAAGC AAGCAGGGTC ATATGGTTAA ACATGGAATT TTTTAAAGGA GTTATTACAA 180
 GTGGGAGTCA AATAGAACTG TGGTAGAATG CTTTGGGTAC AGGAATATGT TATGCAATAA 240
 AGTGAGGAAG AGAAAAAGGG AATAAGAAGG GAGGAATGTA ACTAGAGCAG CTCCCAACAG 300
 TTTGCCTATG TATTTGCCAG CACCAAAATT CGTAGAGTAA GCCACTTACA TTTCCACTGC 360
 TAGTATTAAG GAAAGACAGC AGTGGTGATT CTTATAAAGT GAGTATACAT TTATTCTTAT 420
 TCTGATATGT GAATTTTCTT TTCACCAGTT AATTAAGTGG TAATTTGTAA ACAGTGGGAA 480
 GAAGATTAGA ACAATTATGG AGGTACTGAA TTACACAAGG AGATTAAAT GAAATGAATC 540
 AAATAACCA CAAGATAGGT AGATTGATTC ATTTCATTTT AATCTCCTTG TGTAATTCAG 600
 TACCTCCATA ATTGTTCTAA TCTTCTTCCC ACTGTTTACA AATTACCAGT TAATTAACATC 660
 GTGAAAGAAA AATTCACATA TCAGAATAAA AATAAATGTA TACTCACTTT ATAAAAATCA 720
 CCACTGCTGT CTTTCTTAA TACTAGCAGT GGAAATGTAA GTGGCTTACT CTACAAATTT 780
 TGGTGCTGGC AAATACATAG GCAAAGTGT GGGAGCTGCT CTAGTTACAT TCCTCCCTTC 840
 TTATTCCCTT TTTCTCTTCC TCACTTTATT GCATAACATA TTCCTGTACC CAAAGCATTC 900
 TACCACAGTT CTATTTGACT CCCACTTGTA ATAACCTCTT TAAAAAATTC CATGTTTAAC 960
 CATATGACCC TGCTTGCTTA CTCATATTCT CCCTCCCTCT CCCCTTCCTT TCTCTCTCTT1020
 CCAGAAGTCA TTTGCCTGGT TTGAAATATT TTGTAGGGAT TGCTTATTAT ATTATTTTAG1080
 CTGATGAACC TCAGGACAAC GTCTACACAC ACACACATAC ATACACGCAC ACAAATCTC1140
 AGCTGTTGAA GAGTGGGCTT GGAATCAGAC TTCTGTGTCC AGTAAAAAAC TCCTGCACTG1200
 AAGTCATTGT GACTTGAGTA GTTACAGACT GATTCCAGTG AACTTGATCT AATTTCTTTT1260

 GATCTAATGA ATGTGTCTGC TTACCTTGTT TCCTTTTAAT TGATAAGCTC CAAGTAGTTG1320
 CTAATTTTTT GACAACTTTA AATGAGTTTC ATTCCTTCT TTTACTTAAT GTTTTAAGTA1380
 TAGTACCAAT AATTTCAATTA ACCTGTTCTC AAGTGGTTTA GCTACCATTC TGCCATTTTT1440
 AATTTTATT TAATTTTATT TGCTTGAGCA CACTGATCAA CCACTGAACT GCCTTCTTCC1500
 ATTGTCCTGC AATGATATAA GGGTTACATT TTTGTGTATA TGGCTTTCAT TGGTGGATT1560
 TCAGAGCACT GATACCATAT ATTTTCAGTT TGTTCTCTGG GGGAAATTTCA TTTGCATCTA1620
 TGTTTTATAGC TATCTGTGAT AACTTGTTAA ATATTAAAAA GATATTTTGC TTCTATTGGA1680
 ACATTTGTAT ACTCGCAACT ATATTTCTGT AAACAGCTGC AGTCAAAAAT AAAACACTGA1740
 AAGTTTTTCAT TTTGCAGTGG AAAAAAA 1767

(2) INFORMATION ON SEQ ID NO. 238:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2311 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

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CATCGCCTTC ACCGGCGGGCG GCAACATCGT GGTGGCCACG GCGGACGGCA GCAGCGCGTC 60
GCCCGTGCAG TTCTACAAGG TGTGCGTGAC GTGAGTGAGC GAGAAGTGCC GTATCGACAC 120
GGAGATCCTG CCCTCCCTGT TCATGCGCTG CACCACCGAC CTCAACCGCA AGGACAAGTT 180
CCCCGCCATC ACCCACCTCA AGTTCCTGGC CCGGGACATG TCGGAGCAGG TGCTTTTGTG 240
CGCGTCCAGC CAGACCAGCA GCATCGTGGA GTGCTGGTCC CTGCGCAAGG AGGGACTCCC 300
CGTGAACAAC ATCTTCCAGC AGATCTCCCC CGTGGTTGGC GACAAACAGC CCACAATTCT 360
CAAATGGCGG ATCCTATCGG CCACCAACGA TCTGGACCGT GTGTCGGCCG TGGCGCTGCC 420
CAAGCTGCCC ATCTCGCTCA CCAACACCGA CCTCAAGGTG GCCAGCGACA CACAGTTCTA 480
CCCTGGCCTC GGGCTGGCCC TGGCCTTCCA CGACGGCAGC GTCCACATCG TGCACCGGCT 540
CTCACTGCAG ACCATGGCCG TCTTCTACAG CTCCGCGGCC CCGAGGCCTG TGGATGAGCC 600
GGCCATGAAG CGCCCCCGCA CCGCGGGCCC CGCCGTCCAC TTAAAGGCTA TGCAGCTATC 660
GTGGACGTCA CTGGCCCTGG TGGGGATTGA CAGCCACGGG AAGCTGAGCG TGCTCCGCCT 720
CTCACCTTCC ATGGGCCACC CGCTGGAGGT GGGGCTGGCG CTGCGGCACC TGCTCTTCCT 780
GCTGGAGTAC TGCATGGTGA CCGGCTACGA CTGGTGGGAC ATCCTGCTGC ACGTGCAGCC 840
CAGTATGGTA CAGAGCCTGG TGGAGAAGCT GCACGAGGAG TACACGCGCC AGACCGCTGC 900
CCTGCAGCAG GTCCTCTCCA CCGGATCCTT GGCCATGAAG GCCTCGCTCT GCAAGCTGTC 960
GCCCTGCACG GTGACCCGCG TGTGCGACTA CCACACCAAG CTCTTCCTCA TCGCCATCAG 1020
CTCCACCCTG AAGTCGCTGC TGCGCCCCCA CTTTCTCAAC ACGCCTGACA AGAGCCCCGG 1080

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CGACCGGCTG ACCGAGATCT GCACCAAGAT CACCGACGTC GACATTGACA AGGTCATGAT 1140
CAACCTCAAG ACGGAGGAAT TTGTGCTGGA CATGAACACA CTGCAGGCGC TGCAGCAGCT 1200
CTTGCACTGG GTGGGCGACT TCGTGCTGTA CCTGCTGGCC AGCCTACCCA ACCAGGGTTC 1260
CCTGCTGAGG CCGGGCCACA GCTTTCTGCG GGACGGCACC TCGCTGGGCA TGCTTCGGGA 1320
ATTGATGGTG GTCATCCGCA TCTGGGGCCT TCTGAAGCCC AGCTGCCTGC CCGTGTATAC 1380
GGCCACCTCG GATACCCAGG ACAGCATGTC CCTGCTCTTC CGCCTGCTCA CCAAGCTCTG 1440
GATCTGCTGT CGCGATGAGG GCCCAGCGAG CGAGCCGGAC GAGGCGCTGG TGGATGAATG 1500
CTGCCTGCTG CCCAGCCAGC TGCTTATCCC CAGCCTGGAC TGGCTGCCAG CCAGCGACGG 1560
CCTGGTTAGC CGCCTGCAGC CCAAGCAGCC CCTTCGCTGT CAGTTTGGCC GGGCGCCCAC 1620
GCTGCCTGGC AGTGCTGCCA CCCTGCAGCT CGACGGCCTC GCCAGGGCCC CAGGCCAGCC 1680
CAAGATCGAC CACCTGCGGA GGCTGCACCT TGGCGCTTGC CCCACGGAGG AATGCAAGGC 1740
CTGCACCAGG TGCGGCTGTG TCACCATGCT CAAGTCGCCC AACAGAACCA CGGCGGTGAA 1800

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GCAGTGGGAG CAGCGCTGGA TCAAGAACTG CCTGTGCGGT GGGCTCTGGT GGCGGGTGCC1860
CCTCAGCTAC CCCTGAGCCC AGCTGCCCCCT CAGCTACTCC TCAGCTACCC CTCAGCTGCC1920
CCTGAGCCCCG GCTGCTGCAA GAGCCACCGC TCGCCCTGGA CTCTCCTCGG CGCGGTAAAC1980
CTCAGCCCCG CCTGCAGGGC TGTGTAAGGC CGTGGGCCGG ACGCCTGCGT GACCAGCAGA2040
GCTTCTGAGG AAGCCCCTGC CTTTGTCCAG CTGGGCCCGC AGTCCACACA CCACTCTCCC2100
AGGACCCCCA GATCCCTGGA CCATCTGCAT CCAGAGGACC GTCCGTGACG GCCGGGGGTC2160
CAGGCGGACC TTGTGGTGAC CCGGCTCGGG CGTCTCCTCG GTTTCCTTGC CTCACCCGCG2220
GAGAGCGCTG AACCTGGACA AGCAGCGGCT GGGGAAGGACA GGTCCAATAA ACGCCCTCTG2280
CGCCCAAGAA AAAAAAAAAA AAAAAAAGGG G 2311

(2) INFORMATION ON SEQ ID NO. 239:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1772 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

TGGGCGCTGT AGTCCGGCCG GAACCTGTTT GCGACCCCGA GTCCCATGAC ACCGCTTCTC 60
 CTCACACCCC AGTCCGCAGT GCCCCTCCCC AGCCTCGGCC GGGCCTCCCG GGAGCCGGGC 120
 GTGGCGTTCC AGCTAGTGAG CCGTTTCTCC CCTGGGCTCG GAGGCGGAAG CTTGAGGGGC 180
 GCGGGGAGGA GCTTCGCGTG CGGGGTGAAC GCCCGCTCTA CGTGCTCGTT CTCTTCGCGA 240
 CCGCTGCGCG CGAGCCCCGT GTCCCCACGG CGGGCAGCAG CGCCGGCGGC GGCGGCTGAA 300
 CGCGGAGGGG GCGGAGGGAG CCCGCGGCGG CGGCAGCAGC TACAGCGAAA TGGCGGAGAC 360

CGTGGCTGAC ACCCGGCGGC TGATCACCAA GCCGCAGAAC CTGAATGACG CCTACGGACC 420
 CCCCAGCAAC TTCCTCGAGA TCGATGTGAG CAACCCGCAA ACGGTGGGGG TCGGCCGGGG 480
 CCGCTTCACC ACTTACGAAA TCAGGGTCAA GACAAATCTT CCTATTTTCA AGCTGAAAGA 540
 ATCTACTGTT AGAAGAAGAT ACAGTGACTT TGAATGGCTG CGAAGTGAAT TAGAAAGAGA 600
 GAGCAAGGTC GTAGTTCCCC CGCTCCCTGG GAAAGCGTTT TTGCGTCAGT TCCTTTTAGA 660
 GGAGATGATG GAATATTTGA TGACAATTTT ATTGAGGAAA GAAAACAAGG GCTGGAGCAG 720
 TTTATAAACA AGGTCGCTGG TCATCCTCTG GCACAGAACG AACGTTGTCT TCACATGTTT 780
 TTACAAGATG AAATAATAGA TAAAAGCTAT ACTCCATCTA AAATAAGACA TGCCTGAAAT 840
 TTGGCAAGAA GGGGCAAAAA CGTGACTATT AATGATTGAT AAGCACCAGT GAAGAAGTTC 900
 TAACTTTTAG CATGCTGCAC AGAACTGGT ATAACATGCC TTCAGTATAC TAACACTCAT 960
 ATGCTCAGTT TTGTTTTGTT TTGGCAGTTG ACAAGAAGTT AATTTGCTTT AGTAAAAATC1020
 CCTCATTCCA GCCTTTCTAT ATAAATAGCT CTTTCTTGCT GTTTTAATGT GGTGCACACT1080
 ATAGCCTCAC AAACCTGTTA TTCCAGTGTA ATCTGCAGTG TCGTAACTAA AGTTACTGGC1140
 TTGGTCTTAT TTGCACAGTT TTTGCGTCTT GTTTGCTTCT TGCATCTGAT TAACTAGAAT1200
 ATTTCTCTTT CCCCTTTTTA ATTTGTGATG TCACTTGACC CCATTTATGT GTAGGAGCAC1260
 TACACCATTG GTTTCCAATA CTGCACACAT AAGATACATA CTTGTGTGCA GAAAGTATCT1320
 TCCTCCAGGC TTGTAATACC CTTACATGG AAGATTAATG AGGGAAATCT TTATATTCTG1380
 TATAAAAACA AAAGCAAATT TATATACTAA AATCATTGT CTAAAAATTT AAGTTGTTTT1440
 CAAATAAAAA TTAAATGCA TTTCTGATAT GCACTGATTG TGTGCTCC AGCTTTTTTT1500
 GCTCTCTATG AGTGACTACT TAAGTCACTT GTTGAGAGGG ATTATTTACT AATTATATAC1560
 TTCTCATTCC TGTAAGTCCA TTCCCTTTAA ACAGTGGTGA TATCAAATAT ACTTCCATCC1620
 ATTGAATGGG GTATTTTAA CAACAACAAA AGTGATATAC TAAAAAATGT ATTGCTTAAG1680
 GCTTATTGAA TCATTTTGAA GCACTTTGTG TATTTGAAAA CTGCTTTATA ATCTCATTTA1740
 TTAAAAGGAC TTTCAAAGAT AAAACCAAAA AA 1772

(2) INFORMATION ON SEQ ID NO. 240:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2409 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

TCTGTATCTT	CCTTGCCCTC	AAATACCCTG	AGGTGATAAA	CTGTTCCAGT	TGTAGCCAAC	60
TACCACTGCG	CCCGGCCTTA	AATAAAATAT	TGTAGTCATT	AATGGTGTGT	TTGAATTGAA	120
GAGATACCAG	GAGATAGAGG	TGAAGTGCAG	TACTTTTATT	CTTTAAGAAT	ATAGTCTTTA	180
GCCAGGTGCA	GTGGTGTGTG	CCTGTAGTCT	CAGCTATTTG	AGAGGCTGAG	GTGAGAGGAT	240
CACCTGAGTT	CAGGAGTTCA	AGACCAGCCT	GGGCAACATA	GCAAGTCCCT	GGCTCAAAAA	300
AAAAAAAGTT	TCCCATTTCAT	ATTAACCTCA	TCTTTTAAAA	ATGTCATGAT	TACAAAGTGA	360
AAAGATTTGG	CTTTCTTAGA	GGCTCAATCA	CAGAGGTGAA	AGTGACCTTG	GAAATCATAT	420
ACTCTATCCC	CATGTTACAC	AGATTAGAAA	AACTGAGGTT	ATGGCACTGA	CTTAGGCACC	480
CCCCAGCAAG	GCAACCCAGG	GACTACAAC	GGCAATCCCA	ACTCCTGGGC	TAGGGCTTTG	540
TCTACCTTTT	TTTGCAATTG	CCTCTTAAAG	AGGCAATGAA	TACTAATTCC	TGGCATCAGA	600
AAAAAAAAAA	GGCATGAGGT	GGGAGGATTC	TTTTTTCCCT	GATGGGAAAC	AGTGAATAAG	660
AAAAATCTCA	TCATTTCGATG	GAAGAGGTGA	CTTAATAATT	TTATTAATGA	ATTTGATGTC	720
CCATGTTTTG	TAGTTTTGTT	ATCATTGAAC	CATTGGGGCT	GGAATCTGCC	TAAATAATTT	780
TATCTTGGTA	GCCAGCAATT	ATGTTGGTAT	TTTATGTGGG	CCTTCCCAGA	TTTTCATATT	840
AATGAAATGA	CTAATAGTCG	TACTTAAGAG	GTAACCTCTAC	TAAAGCAGAA	TGAGATCTAA	900
TATGTTGTGG	AAATAAAAGA	GTTTGCAGTG	GAATGATACT	CTCACTCCGT	GCTTGTAATA	960
TTGAGTTCTA	TTCAAGACGG	AACTGCTATG	ACTGGCCTAT	TCAAGGCTTC	ATATTTTTTAT	1020
ACAGACTATT	TCACAGACCA	TAGATTTTAT	TTAAAAGGGA	AAATCTCACA	CATAATTAAG	1080
CAGTGAAAAA	TGTGCTCAAT	GCTATGGTGC	GTCAGGCCCT	CTGTCTACCA	GGTTTCTCCC	1140
GCTTTCTGCA	GAGCTGTGGA	CCCTGTACGT	ACCAAACAGG	TGAACTTGGT	CCATCTTTCC	1200
TTCTTCCTTT	TTTGCACAT	TTGCATTTAT	ATCTTCCTGT	ACTAAAAGAA	ACAAATTTATT	1260
TATAATTGGG	GTGACAATAT	AAAGGAACAA	AAGATGGGGC	AATAGTTGCT	TCCTAGCTGG	1320
AGCTTAAGT	CCATGTTACA	GAAACTCACT	ATTTAAAAAG	TTTTAAAAGA	TTTATGAACC	1380
TTGTCCTACA	ATTCGCTGAA	TACTTATTTG	TCTTTTAAAC	TCCCCTCGGT	GTATGGATCA	1440
TCTTCGTCAG	AATGCCGTTG	TTTCATTGTG	AATCAGGGGA	AAATGTTAAT	CATTTGGAGA	1500
CTGTTTTCTT	ATTACCAAAT	GTACAATCCA	TAAGACAAC	GAAAGCAACA	ACTGCTGGGT	1560
TCACTGACAA	AGATTATAAA	AATCATCACG	TTCAAAGTAG	AGTTTTTAGC	CAAGGTCAG	1620
AACTAACCTG	GGGCTGAGTC	AGCGTCTCTA	CCCCTTAAA	TAACAGCGTA	AAGATCTTTC	1680
ACTAAATTCG	TTATGTGGTC	TGTCTGGATG	TAAACCTATA	TATTTCCCTT	TGAAACAGAA	1740
TCATATCCTG	CAGACTCTTG	GCACTCCTGC	ATAGCTTTGA	CCGAATGTTT	ACTCTCATCG	1800
TAATGGAAGA	TTTCTATCTA	TGCAGATAAT	ACATGTTTTT	AAATACTGTT	TTCTGTTTAG	1860
TCCTCAATCT	TCCTAACTCA	AATTGGGGAC	TGAGGAGAGA	GAAAGGTGGT	TACCCCTGTT	1920
ACCGTGCCAT	ATTCTTCTTG	CTGCTTTTCA	ACCCACGCTG	ATTGTTGATT	GACGGTCTG	1980
CTATAATGTG	CGTGCCCTTC	AAGTTTCAGA	AACTTTCCC	AATCATTTCA	CTTCAATCTT	2040
AATTGAACCC	AAGAGTCAAA	GTTATTATTT	TCTCCGAACG	TGTTTGTGAT	CTTCTGTTAT	2100
ATTTTGGGGC	ATGTTACCTT	TATGGTATAT	AAGCTGTAGT	GCATACTCTT	TGTATTGCAA	2160
AAAACCTGGT	AGTAATTTAT	GTACATGTAT	TCCACATTTT	AGTGTGCTTG	AAGTGACAA	2220
CCATAGTTTG	TAGTAGTTTG	TTATTTGTCA	ACTTTACCCT	GTGTTTTTAA	GACATCTAAA	2280
CATTCCCTGT	CCTATCAAGA	TGACAAAAGC	AGAATGTAAT	TTTTTTTTTG	AAGCTTCGTG	2340
ATTACCTGTA	ACAAGTTCTG	TTTTTAAAAC	GAATACAAAT	AAAGTTAGTA	ACTATTTTAA	2400
AATCAAAAA						2409

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2594 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

CGCCCTTTTT	TTCTTTATTT	TCTTATGTAC	TCATCTACTT	ATTCTCAAAG	TATTTAGCAT	60
TCAACACTCT	TTTTGCTTTT	AAAAGAATGG	CCTTACAAAG	GGACAGAAAA	GAGAAGACAC	120
GAGCTTGGTG	TATTTTCATC	AAGTTATGTG	GCAGAGAAAT	CCAGATATTA	CCAGGACCTG	180
TCTAAACAAA	TGTTGTGGGT	TTTCTTTTCA	TTCGGATAGC	CACTTTATAG	TTGGAATATC	240
AATTCTAATG	AGGAGGAAGA	CATAAATATA	AGTGGTAAAA	AGAAACATGA	CTTCCCTTAA	300
AACAGGCTGG	ATAATCTATA	TCAGCCTTGT	GGGTGGAGAC	TAGTATTTGA	TCCTTGCCAT	360
ATAAAACATT	TTAATATGGT	TTACATGGGA	AAATATCGAT	GGCTTCCTCA	CAAAATGTAT	420
GGGTGACGTG	AAGTTGAAGA	GCCAATGGCT	TGGGTGACAC	GTGCTGGATC	CAAAAAGATC	480
AGGGAGACTA	GAATAAACT	TGGATGTTAA	AAATTCACCA	GGAATCCACA	TAAAGTACTA	540
TATTTGGGCT	AAAATGAAAA	ACTAAATACA	AGGTGGGAGA	GAGGCAAGAA	TTTCAGTTGA	600
CTAAGCTCAG	TGTGAGTTCA	AAGTGGGATG	GAACCATGCA	AAAACAAAAC	CCACAGACAT	660
GCAGGCTACG	TGAGGAGAAA	ACAGTGGTGA	GGATCACATC	ACATTGTGTT	TGCATTTGCC	720
GGAACCATAC	TTTAAGAAGA	AAACCGATCA	TCTATAATAA	CATCAGTTTA	TCAATGCCCC	780
GTCCTGATGA	AGTGTGCAGA	CTCTCAGAAA	CAGCAGGAAG	GACTTCATGA	GAACCCTCAG	840
GCTGGAGAAG	GGACTAGGGC	ACAAGGAGAG	CTCTCCTAGG	ACCAGGACCA	AGAAGCTACA	900
GGCAGGCACA	GTTTAGCTCC	TGCAGAGACC	CAGCTTTTCA	CAAGTTGGAG	CCTTCCAGAG	960
ATAGAGGGAC	TGTGGTAGGT	GGTGACCCAC	CCATCACTGG	AGGTGGAAGC	AGAGGCCGTT	1020
TGCCAGGGAT	GCTGGAGAGG	GGATTCAAGC	ATCTGGCTGG	GCAACGTGAT	GCTCAGGGCC	1080
GTCTCCACTC	AGGGCTTAGG	GGAGTCTGTG	AGTAGAAGAG	CTTTAGGTGA	TTTGTGTTGG	1140
GGGGGAAGGC	AAGTACACAG	CTATGCACTT	TCCGTTTCTG	ACTTTTGCCA	CCCTGTTCAGC	1200
CATGGGGAGC	CCACTGTGGG	ACTGAAACCC	TGAGCTGAAT	GCGGCCTCAT	GTCTCAGAGA	1260
AACACTGGCA	AGTTGGTCAG	AGCCGCCGTC	TGCATCGAGG	CGTACTGAGC	GGCAGGATGG	1320
GGGGCTGCCT	GCCCAGGGTC	TCTCACC GTG	GTGTAAGCAG	AGCCATGGCT	TGCCTAGGAC	1380
CCTATAGATA	CCATCACTCT	TTCTCAGCTC	GACTGGAGTT	TCTGCACCTT	TGCAGGGGCA	1440
AAGTAACTCC	CTGCACCCTG	AACCACCCCC	CATTCTGT	CATTTTCAGCA	GATAATGATG	1500
GAGGGGGGGG	GGTGTCCATC	GTGCTGAGGG	TGTGACCGCA	AGAGGGTGAA	AACTTCCAGC	1560
CAACTTTCTC	AGTCCTTTCT	CTTGCGAGAG	GGAAGCCACC	TGCTATACAA	ACTAATACCC	1620
CCTGCCTTGA	CCCCTTCCCC	ACGACTCAGT	TGACAGAAAG	ATATACTTTG	TTATAACTTA	1680
TTATTTTGTT	CTCTGTAAAT	ACAAGATGTT	TATAGGAAAT	ATGTATTCTG	AACTCTATCT	1740
GCAGAATGAG	TCACTACACC	AAAATAGTTC	TATTATTTAG	AATGTGTTAA	TTTTAAAGGG	1800
ACCTGATAGG	TATTTATTTA	CATATGCGAT	CCACATTTGT	GTGAAAGCAT	GTGATCATAG	1860
TAACCCAGCC	TCCTGGAATG	TCGCTGTACG	ATGATTGATG	TCTTTTTTCTC	AGTCCATAGT	1920
TACAATTGTT	TAGTATGCTA	ATCAGTCCAG	TTCCCTGAGG	TTTAAGATCA	AATATAAAAT	1980
ACTCTGCTTT	TCGACTCATT	CAGGTAGCAT	TGTACCTGAA	CCTGATTGCT	ACTTTTTTCAT	2040
CTTAAATATT	ATATTTCCCTC	ATCTAATCTG	CCTTCCCCCTC	ATCCACAGAC	ATTTGGAGAA	2100
GGAAATGGGA	GGGTGTCTGT	TATCCCTTTC	TCTTTGCTTT	GTCCCCGTTG	TTAGACTGGC	2160
AGCGTCAGTT	GCTCGGTGGG	CTTGTTTAGA	GCCGTGGGTG	AGGCAGGTGG	CTGGCGGGGA	2220
CAGGGAGAGG	CTGAGAGGGA	AGTGTGGCA	TTTACTGCTC	TGACACTTCC	ACTGTCCCTG	2280
CTGGGGATGC	TGGGGCCAAG	GCCTGTGGGG	CCTGTGAAC	GCACAGCCAG	GAGCAAGGAA	2340
CCCCTAAAT	ACTCCGTCAC	CTCCATGTCC	CCTCTACAGT	GTTAAATTAT	TACATAAGCA	2400
GGTGAAAGGT	AGAAGGCGAA	TTATGTGAGT	AAATATGGTC	TGTTTTCTCT	TCAGCAAAAA	2460
TGACTATTTT	TGTGTGTGAC	TAATTTATTT	TTATTATTGT	AAAGATACAA	TAAACCGGTT	2520
GAAATATCTG	CTTTGTTGAC	AAGCGTGTGC	TTTCTATGGC	NTTATTNGCG	TTCTGTTNTC	2580
CTGNAAATAG	CGCC					

(2) INFORMATION ON SEQ ID NO. 242:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1012 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

TGAAGTGGAG AGGTGAAGGT TGCAGTGGCC TGAGATCGCG AAACAGAGCG AGACTCCATC 60
 TCAAAAAATA AATAAATAAT AAAATTGGCC GTTCACGGTG GCTTATGCCT GTAATCCCAG 120
 CACTTTGGGT GGCCGAGGCG GGTGGATCAC CTGAGGTCAG GAATTCGAGA CCAGCCTGAC 180
 CAACATGGAG AAAACCCCGT CTCTACTCAA AATACAAAT TAACCGGGCG TGGTGGCGCA 240
 TGCCTGTAGT CCCAGCTACT TGGGAGGCTG AGGCAGGAGA ATCACTTGAA CTCAGGAGGC 300
 AGAGGTTGCA GTGAGCTGAG ATCATGCCAT TGCCTCCAG CCTGGGCAAC AAGAGTGAAA 360
 CTCCGTCTCA AAAAAAAAAA AAAAGAGATG TTTTTCATTT TTTTCATGTT ATCTATCCAA 420
 GCACTGTTCC ATGGTCAGCA AGTCATATTT CATAATGTGG ATTTTCCAAA ATAATTATTG 480
 AATACAGCTA TTCTATGGCT ACTTTTAGTG TTTTGTGGT ATGTGGTGTG GGAGTGTTTA 540
 TGGAATTACC AGTATCTTAA ATTTTCAAAG GAACCTTGGA AGTCTATCAC TCTAAATGAA 600
 AGTCTGTCAC TCTACATGAA TTATGTGCTC AAATTTGACC AACTCAGTTT AAGACACAAA 660
 ACAGTAATTT GAAGAAGGAA AAATGAAGAG AGTTTCTAGT TTAATGGGTT AAATTTTGT 720
 TGTTGCAATA GTAAGTTTAG TCTTCTTATA ATATTTCTAA ATGAAAAATC ATAGGTATTT 780
 GTTACCATGT GTGAAGATTA CTTTGTTAAA AGCAAAAGTG GTCGTGTGAT ATGCTAAATG 840
 TTAATTACTG ATTTTATATG TTAAATCAC GCCAAACAAA TTATGTCTGT GCCATCCAGG 900
 GTCTGTTGTT AATCTTTTTC TGAGTACTTG GATTGGGATA AAGGGCTTGT ACTATGCACT 960
 TTTTATTAAT GAATAAATAG AAAACGTTAG TAACAAAAAA AAAAAAAAAA AA 1012

(2) INFORMATION ON SEQ ID NO. 243:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

TGAGACGGAG	TCTCGCATCT	GTCGCCCAGG	CTGGAGTGCA	GTGGCGGGAT	CTCGGCTCAC	60
TGCAAGCTCC	GCCTCCCGGG	TTCACGCCAT	TCTCCTGCCT	CAGCCTCCCA	AGTAGCTGGG	120
ACCACAAGCA	CCCGCCACTA	CGCCCGGCTA	ATTTTTTGTA	TTTCTAGTAG	AGACGGGGTT	180
TCACCGTTTT	AGCCGGGATG	GTCTCGATCT	CCTGACCTCG	TGATCCGCCC	GCCTCGGCCT	240
CCCAAAGTGC	TGGGATTACA	GGCGTGAGAC	CGCGCCCCAC	ACTATGAGTG	TTTTTAACAC	300
CATTCTCCCC	CACTTCTCTC	CTGGGTGACA	TAAGAGAGAA	ATAACCNTGT	AGTACAGCAG	360
CTAAAGTATT	CTCCTTTCAG	AGAANNTTTT	TTTGGAGGTC	TCTAATATAT	ATTTCCCCCN	420
TTGTCTCTGT	GATCTCTTAT	TTATACTATA	TTATTGTCCC	ATGTACTTTC	TAAACTGAGC	480
TTGGAACATT	TAGTATTCCT	GCAATTGGAC	TTCCCACTTA	ACAATTATAC	AGACTTTGCT	540
TTTAGAAATA	GATTAGGTTC	CAAACAGAAA	GTTTNAANGT	GTAACAACNA	ACAATAAAAA	600
TAGATTATGA	AACANGGCTA	TAATTGGCTC	TTTTGGATTT	NGATAGGGGC	AAGATGAAAG	660
GNCAACNTTT	CTTGCNTTTT	GAAANNTCAT	NGTTNGGGTA	ANGAGGTAAG	GNAATNCCAG	720
CTANCAATTT	TNATTAGTGC	TTGNAAANCG	GGCTTNCCTT	NGAATTCNTC	CANGGNCCCT	780
ATCATTTTTT	TTTTCTTNAC	TAATNCAGAA	GAGAGNCTGG	GGTAGAAGNC	CCCATNGTTT	840
GTATTCCNAT	GAAACACNGT	CGGGTTGGNA	GTAAAGGCAA	AAACAGCNTA	GACACACCAG	900
GNTGTGTCTG	NNTTTGACAT	TTATAAGCTG	GCACTCATCA	ACACTCCTGT	TTCTCCTTTC	960
TCTGGGACGT	GTGGATTAAG	GGGTGTGAGT	TGTGGGAAGA	ATTGNCCCTC	GTACCTCCTG	1020
GATTTATTAT	TTTTCTCAAA	TACCAACCNA	GTAAGATCCC	AAATAACTTG	AGAAAAATTG	1080
TTTCCTGATC	TGTCCACTTC	TGGTGTCAAA	GATTTTACTC	ATCTTCTTAG	TACATTCTAT	1140
GTATTTTATA	TGTATAATTT	TNATACAATT	AAAAATAGAT	TTTTGTNCTA	GTNGAAAAAA	1200
AAAACA						1206

(2) INFORMATION ON SEQ ID NO. 244:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2514 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

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AAGGTGAAGA GCGGCATCCG GCAGATCCGG CTCTTCAGTC AGGATGAGTG CTCCAAGATC 60
GAGGCCCCGA TCGATGAGGT GGTGTCCCCG GCGGAGAAGG GCCTGTACAA CGAGCACACG 120
GTGGACCGGG CCCCCCTGCG CAACAAGTAC TTCTTCGGCG AGGGCTACAC GTACGGGGCC 180
CAGCTGCAGA AGCGCGGGCC GGGCCAGGAG CGCCTCTTAC CCGCCGGGCG ACGTCGACGA 240
GATCCCGGAC TGGGTGCATC AGCTGGTGAT CCAGAAGCTG GTGGAGCACC GCGTCATCCC 300
CGAGGGCTTC GTCAACAGCG CGGTCATCAA CGACTACCAG CCGGCTGCT TCTTTAGCGA 420
CCACGTGGAC CCCATCCACA TCTTCGAGCG CCCATCGTG TCGCTCTCT TCTTTAGCGA 480
CTCTGCGCTG TGCTTCGGCT GCAAGTTCCA GTTCAAGCCT ATTCGGGCT CGGAACCACT 540
GCTTTCCCTG CCGGTGCGCA GGGGAAGCGT GACTGTGCTC AGTGGATATG CTGCTGATGA 600
AATCACTCAC TGCATACGGC CTCAGGACAT CAAGGAGCGC CGAGCAGTCA TCATCCTCAG 660
GAAGACAAGA TTAGATGCAC CCCGGTTGGA AACAAAGTCC CTGAGCAGCT CCGTGTTACC 720
ACCCAGCTAT GCTTCAGATC GCCTGTCAGG AAACAACAGG GACCCTGCTC TGAAACCCAA 780
GCGGTCCAC CGCAAGGCAG ACCCTGATGC TGCCACAGG CCACGGATCC TGGAGATGGA 840
CAAGGAAGAG AACCGGCGCT CCGTGCTGCT GCCACACAC CGGCGGAGGG GTAGCTTCAG 900
CTCTGAGAAC TACTGGCGCA AGTCATACGA GTCCTCAGAG GACTGCTCTG AGGCAGCAGG 960
CAGCCCTGCC CGAAAGGTGA AGATGCGGCG GCACTGAGTC TACCCGCCGC CCTCCTGGGA 1020
ACTCTGGCTC ATCCTTACGT AGTTGCCCCC CTTTTTGTTC TGAGGGTTTT GTTTTTGTTC 1080
ATTGGGGGGT TTTTGTTCCT TGTTCCTTGT TTTTTTTGAT TCTATATATT TTTCTTGGT 1140
TTTGTTGCCT GTTAAGGCTG AAGAATAGAA TTGGCCAGGA CCTAGGTTCT CATATTCTTG 1200
GTATTCCTCC TGGATGGAAA GGCTGTTGGC ATCAATAGGG GACAGAGGCT GATGCTGGAG 1260
TGGCCAGTAG AGGTGGTGGA GCAGAGCAGC CATCTTTTAA GTGGGGCTGT ATCAGGCTGG 1320
GTTTTATTTA AAGCAACAAA ATGTTTTGGT TAAGAAAATT ATTTTGCTTT CAGTGTAAT 1380
CTTCGCAGTG TTCTAAACAA AGTTCAGTCT TCTGCTCGCC CTTTTCCCTC ACTGATGTCT 1440
GCACTTGGTT GAGGTCTCCT GGAGCCTCAC AGGCTCTGCT GTTCTCCACT TCTCACCTGC 1500
CATCCACGCC CTGCAAGCTC ATGCAAAACAC CTTTTCTTCC TCCTGCGGCA GAGTTGTTCA 1560
GGTTGCCTGG GCAGGGGCTT AAACAGTGCC AGCCCCTGCC ATCCCAAAGC TATTGTTAAG 1620
CCCCCCAGGC GTCTCCACC CACGCCCCACT AGCCTGCCAT GTCCACAGTT CCTTGGGCTG 1680
CTGAGGGGCT AGTGCAAGTG TCCTGACCTC TCTTATCAAG AGCACACTTC TTTGCTGGTT 1740
GCTCCTTTTG AGCATATGCG TGTGATTATT TGGAACAGTT AGACTTGCCA CGTTGGGTCA 1800
GTTTTAGAAA TTGTTTCTAG CTAGAGGGAC TGGTGTCTCT CCAAGTCTAG CATTTGGGGT 1860
ATGGAAAATT GTTGTGGTGT GTGGTAGGGT TTTTGTTCCT TTTTGTGAGT TTTTTTCCC 1920
CCTTTAGTCT CCTGGCTTTT TCCTTTCCCT TCCCTTCTCC ACTGGCCAGC TTGGGCCTCA 1980
TCCTCATGTC ATCCTTCTAG GAAGGCGCCT GCCCCATCTT GTCTGCCGCG AGCATGCATC 2040
CAAGGCCAGA GCTCAGGCCT GCAGACTGGG CTGGTGCCCT CTCCGCTTCA GGGTATGGGA 2100
GTTGGTGAAG GGGCTTTCAA AAAATAATAA GAAAAAAAG GTAAAGTCTT TGGTAGCTTC 2160
TATCCACTCA GATCCTGGAA GGCAGCAAGG TTTTGTGGAT CTAGATTCAT TAGGAATGTC 2220
TTCTTGTCAG CCAGGCCAGG ACCCGGGCTT GCCAAGAGCA GAGGCCCTCC CAGCAACCAG 2280
GATACCACCA CTTTGGGGGC TTTGTGTACA GAGGTCCGGG TCTGAGACCT CATAGGCTGC 2340
AGAAATCTGG GGCAGCCACC ATCAAGAAGC CCCTCTCAGG GGCCAGAACT CCTTTGCCAG 2400
CGTGGATTTT TCAAGTCGGG ACTGCATAAT TAAAGCAGTT GCAGTTTTAT TTTTTTTACA 2460
GCTTTTTTCC CAAAAATGAT TTGTAGTTGT GTGTGCAGCA CTTCCGCCCT ATATGTGTGC 2514
TCTACAATAA AAACCAATC TAATATATTT TGAAAAAAA AAAAAAAA

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(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 3903 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

GCAGTTGGAT CCCTGGCGGG TCGGGCCCGG CCCGGCCCGT GAGCGGCGCA CAGAATGGGC 60
 CGATGCTGCT TCTACACGGC GGGGACGTTG TCCCTGCTCC TGCTGGTGAC CAGCGTCACG 120
 CTGCTGGTGG CCCGGGTCTT CCAGAAGGCT GTAGACCAGA GTATCGAGAA GAAAATTGTG 180
 TTAAGGAATG GTACTGAGGC ATTTGACTCC TGGGAGAAGC CCCCTCTGCC TGTGTATACT 240
 CAGTTCTATT TCTTCAATGT CACCAATCCA GAGGAGATCC TCAGAGGGGA GACCCCTCGG 300
 GTGGAAGAAG TGGGGCCATA CACCTACAGG GAACTCAGAA ACAAAGCAAA TATTCAATTT 360
 GGAGATAATG GAACAACAAT ATCTGCTGTT AGCAACAAGG CCTATGTTTT TGAACGAGAC 420
 CAATCTGTTG GAGACCCTAA AATTGACTTA ATTAGAACAT TAAATATTCC TGTATTGACT 480
 GTCATAGAGT GGTCCCAGGT GCACTTCCTC AGGGAGATCA TCGAGGCCAT GTTGAAAGCC 540
 TATCAGCAGA AGCTCTTTGT GACTCACACA GTTGACGAAT TGCTCTGGGG CTACAAAGAT 600
 GAAATCTTGT CCCTTATCCA TGTTTTCAGG CCCGATATCT CTCCCTATTT TGGCCTATTC 660
 TATGAGAAAA ATGGGACTAA TGATGGAGAC TATGTTTTTC TAACTGGAGA AGACAGTTAC 720
 CTTAACTTTA CAAAATTGT GGAATGGAAT GGGAAAACGT CACTTGACTG GTGGGATAAC 780
 GACAAGTGCA ATATGATTAA TGGAACAGAT GGAGATTCTT TTCACCCACT AATAACCAAA 840
 GATGAGGTCC TTTATGTCTT CCCATCTGAC TTTTGCAGGT CAGTGTATAT TACTTTCAGT 900
 GACTATGAGA TTGTACAGGG ACTGCCTGCC TTTCCGGTATA AAGTTCCTGC AGAAATATTA 960
 GCCAATACGT CAGACAATGC CGGCTTCTGT ATACCTGAGG GAAACTGCCT GGGCTCAGGA1020
 GTTCTGAATG TCAGCATCTG CAAGAATGGT GCACCCATCA TTATGTCTTT CCCACACTTT1080
 TACCAAGCAG ATGAGAGGTT TGTTTCTGCC ATAGAAGGCA TGCACCCAAA TCAGGAAGAC1140
 CATGAGACAT TTGTGGACAT TAATCCTTTG ACTGGAATAA TCCTAAAAGC AGCCAAGAGG1200
 TTCCAAATCA ACATTTATGT CAAAAAATTA GATGACTTTG TTGAAACGGG AGACATTAGA1260
 ACCATGGTTT TCCCAGTGAT GTACCTCAAT GAGAGTGTTT ACATTGATAA AGAGACGGCG1320
 AGTCGACTGA AGTCTATGAT TAACACTACT TTGATCATCA CCAACATACC CTACATCATC1380
 ATGGCGCTGG GTGTGTTCTT TGGTTTGGTT TTTACCTGGC TTGCATGCAA AGGACAGGGA1440
 TCCATGGATG AGGGAACAGC GGATGAAAGA GCACCCCTCA TTCGAACCTA AACATTGCCT1500
 TTGCTTGGTG AAGAACTGT GTGAGCTGTC CTGACCTGGA CGATGACGTG GGGAAACCTT1560
 CCACCTCCTT GCAGGCTTGT TGCCTGTTGA AAGAAGGAAA AAGACACGGC GCTGGCAAGT1620
 GATAGGAACA TTCTGGCCAG AGGTTAAAGA GCAGGCTGAC ATGGCTGGCC ATTAAGCTTT1680
 ATAAATCAT GTGGGCTCTG AAATTGTTCT TTTATGTGTC TAGCAAGTAT TTAATAAACC1740
 CTTGTATAGT AAAAAAAAAG TTGTTGGGTG CTGGTAGCTC CAGAATTTTG TGACCACTAT1800
 TGTGGGTAAA ATGTCTCTGC ATCACTTGTT AATGCTACTG GTCTAACTTC ATTCAAGTAT1860
 CTTCAATCAC CGAACTTTGT GCTCAAAATG CGTATATACC ATTTTATGTT GTATTCCTCC1920

ATTTCACTTG CAAAACAGAA GTAAATAAGA GTTCGGGACC CAGGGTAAAA TGGTAGCTTC1980
 ATCCAATATA TCATTCAAAT GCATCTGATT TCTAAAACAT ATTACATTTT ATGCTGATCT2040
 TCAGTTCATA ATTCTTCCAG GAAAACTCAG TCTTCCAAC GCAATAAAAT ACTGGGTAGA2100
 ATCAAATGGG AAAGGGGTTG GGTGGGGCAA TACCCATGAG TTGATAGTGA TAAGCTCCTA2160
 AGGATTTTTA ACTTGACTT TTGTGAACGA AGAGAATGCA TAAATAATGT TGGTGAGGAT2220
 AAAGTACAGA TATTTTCATGT AGAATTAATT GCTAGTTATG ATGCTTGTGG ATAGTTAACT2280
 GTTTTTTTTT TAGTCAAAAT GATCATGCTA CGAAAAGATG CTTCTGAGAG AATGTAATGA2340
 GTAAC TGATT TTTCTTCTG AGTCGCCCTT GCCAAATATG TTAGTGTATT AATTAATCTA2400
 ATATTGAGTG ATTATTTGTA AAATTATGAA TATGGGAAAT CCATCTATCT ACAGCCTAAG2460
 TTACACATAA GTTTTCAGAAA GTCTGATTAG ACTAAAGAGA TATTTCTTCT GGGACAGCCT2520
 TCTTCTTGGT AATTTTGAAG TTCTTTTAC AAGTTCCTTC CTCAGTTTCA GTTCTTTCCA2580
 GTGTTTTGTA GCTCACTGTC ACTCACTGAA TAGAGAAACG TGTGCCCTAT ACTTCCTGTG2640
 ACAATCATTT TGCTGACAGA ATGATGGATG TTTAAATAT TGCACAAAGT ACTTTAAAGA2700
 AAGGTCTGTT AGGACCAGAA GCAGAGACAC CACTTTTCAA AGGACTTCTT GGTTCAGCA2760
 TAACCTAAGA CAGGGAATTG GGAGCCATCA TATGTCACAG TGTTTCAAGT TCAAGCATAT2820
 TTAAGGGCAT TTTCTTTGAT TCTCAAAGTT CAGCATTCAT TTTGAATTGA GAAGCCTATA2880
 CATTTAGCTG ACAAAGTGCT TATAGAATTT CTTAACAAC GAACCATTCA AAAGGATTTT2940
 TTTTGTTTTAA AACTGGATTT CAATGTAAGC AAATGAAGAA AAAATATAGA TTTCAATTTCC3000
 ATAGCTTCTT ATCCCTGTAT TGAGGTAATA AATTGTTTTA CTGACAATTT TTCTTTTTTC3060
 TACACTAAAA CAATATGTGA TATATTTCCC CTCTTGAAGA GGCAATTCAT TAAACTCTCA3120
 AATTTTCTAT AGAATCAAGA TAGAACCTTT AGATACTCCA ACTCACCAAA ATGTAAAAAA3180

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ACTAACAAAA ATATTTGGTC TTCAATAATG CTAAATATCT ACATTTTATG AATTTATCAA3240
CATTTAACTA GATAATTGGG CATGTCTTAA TTATGCATGT ACTTATCCAT ACTAATAAAA3300
TTGACAATGC TAGTGCATAC TTATTGGTTT AGTCCTATTA TCAGGATATA ATCATCTGTG3360
AGGAGGATAT TTTAAATACT GTAAATGATA ACAGTTAATG ATATACACAT TTAGACTGAG3420
TTGCACACTG GCAGGGAGAC CAAAAACATT ACTTCCATAC TTGTGTCATG ATTCTTTTTT3480
TTTTGAGAGA GTCTCACTCT GTCGCCAGGC TGGGAGTACA GTGGCATGAT CTCGGCTCAC3540
TGCAACCTCT GCCACCCCAG GTCCAAGTGA TTCTTCTGCC TCAGTCTCCC GAGTAGCTGG3600
GACTACAGGC ACCCACGAGC ATGCCTGGCT AATTTATGTA TTTTGTAGTAG AGACGGGGTT3660
TCACCATGTT GGCCAAGCTG GTCTCAAACCT CCTGACCTCA AGTGATCCAC CCACCTCAGC3720
CTGTCGAAGT GCTGGGATTA CAGGTGTGAG CCACTGCGCC CACCTTCTAT TTTCATCTTC3780
TTTTTAAGGA ATTAATTATT TGAATATGGC AAACATCCAC ATGGGGGCCTA AAGTCAAATA3840
ATGTAAAGCG ATACATTAAA AGGGCTTTAC TTCCACCTC TTTAGGTCTT AATTCAGTCA3900
GTT

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(2) INFORMATION ON SEQ ID NO. 246:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1730 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

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GCATTTCTGC CATCGCCAC CGTGGCGGCA CAAGCGGCAG CCCGAGAACA CGCTGGCGGC 60
CATTCGGCAG CTAAGAATGG AGCAACAGGC GTGGAGTTGG ACATTGAGTT TACTTCGGAC 120
GGGATTCCCTG TCTTAATGCA CGATAACACA GTAGATAGGA CGACTGATGG GACTGGGCGA 180
TTGTGTGATT TGACATTGTA ACAAATTAGG AAGCTGAATC CTGCAGCAAA CCACAGACTC 240
AGGAATGATT TCCCTGATGA AAAGATCCCT ACCCTAAGGG AAGCTGTTGC AGAGTGCCTA 300
AACCATAACC TCACAATCTT CTTTGATGTC AAAGGCCATG CACACAAGGC TACTGAGGCT 360
CTAAAGAAAA TGTATATGGA ATTTCCCTCAA CTGTATAATA ATAGTGTGGT CTGTTCTTTC 420
TTGCCAGAAG TTATCTACAA GATGAGACAA ACAGATCGGG ATGTAATAAC AGCATTAACT 480
CACAGACCTT GGAGCCTAAG CCATACAGGA GATGGGAAAC CACGCTATGA TACTTTCTTG 540
AAACATTTTA TATTTGTTAT GATGGACATT TTGCTCGATT GGAGCATGCA TAATATCTTG 600
TGGTACCTGT GTGGAATTTT AGCTTTCCCTC ATGCAAAAGG ATTTTGTATC CCCGGCCTAC 660
TTGAAGAAGT GGTCAGCTAA AGGAATCCAG GTTGTGGTT GGACTGTTAA TACCTTTGAT 720
GAAAAGAGTT ACTACGAATC CCATCTTGGT TCCAGCTATA TCACTGACAG CATGGTAGAA 780
GACTGCGAAC CTCACTTCTA GACTTTCACG GTGGGACGAA ACGGGTTCAG AAAGTCCAG 840
GGGCCTCATA CAGGGATATC AAAATACCCT TTGTGCTAGC CCAGGCCCTG GGGGAATCAGG 900
TGAATCACAC AAATGCAATA GTTGGTCACT GCATTTTAC CTGAACCAAA GCTAAACCCG 960
GTGTTGCCAC CATGCACCAT GGCATGCCAG AGTTCAACAC TGTGCTCTT GAAAATCTGG1020
GTCTGAAAAA ACGCACAGA GCCCCTGCCC TGCCCTAGCT GAGGCACACA GGGGAGACCA1080
GTGAGGATAA GCACAGATTG AATTGTACAA TTTGCAGATG CAGATGTAAA TGCATGGGAC1140
ATGCATGATA ACTCAGAGTT GACATTTTAA AACTTGCCAC ACTTATTTCA AATATTTGTA1200
CTCAGCTATG TTAACATGTA CTGTAGACAT CAAACTTGTG GCCATACTAA TAAAATTATT1260
AAAAGGAGCA CTAAAGGAAA ACTGTGTGCC AAGCATCATA TCCTAAGGCA TACGGAATTT1320
GGGGAAGCCA CCATGCAATC CAGTGAGGCT TCAGTGTACA GCAACCAAAA TGGTAGGGAG1380
GTCTTGAAGC CAATGAGGGA TTTATAGCAT CTTGAATAGA GAGCTGCAAA CCACCAGGGG1440
GCAGAGTTGC ACTTTTCCAG GCTTTTTAGG AAGCTCTGCA ACAGATGTGA TCTGATCATA1500
GGCAATTAGA ACTGGAAGAA ACTTCCAAAA AGATCTAGGG GTATGCTCAT GGTGCAAAGT1560
GGGGGAAC TA AACTCTTAGG GGAGAAGAGG GGGTGACCCG CAAAAGAGAC GAGATTAGAG1620
GGAACGAGAG GGGGAAGCCG GAGAGTCCAG GAAATAAGGA GGTGAAGAAA GAAGGTTGTT1680
TAAGGCGAGC TGGGGAAGTT GGAAGCCCGA AACTTGAAAG GAGGATAAAA 1730

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(2) INFORMATION ON SEQ ID NO. 247:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3439 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

CAGATTTTGC	CGGCTTTTAT	CCTTTTATTT	AACGGATTGA	AAAGAGCATA	TGCCTGCCAT	60
GCAGAACATG	AAACCGAGGA	ACTGGGGAGT	GATGAAGATG	ATATTGATGA	AGATGGGCAA	120
GAATATTTGG	AGATTCTGGC	TAAGCAGGCT	GGTGAAGATG	GAGATGATGA	AGATTGGGAA	180
GAAGATGATG	CTGAAGAGAC	TGCTCTGGAA	GGCTATTCCA	CAATCATTGA	TGATGAAGAT	240
AACCCTGTTG	ATGAGTATCA	GATATTTAAA	GCTATCTTTC	AAACTATTCA	AAATCGTAAT	300
CCTGTGTGGT	ATCAGGCACT	GACTCACGGT	CTTAATGAAG	AACAAAGAAA	ACAGTTACAG	360
GACATAGCAA	CTCTGGCTGA	TCAAAGAAGA	GCAGCCCATG	AATCCAAAAT	GATTGAGAAG	420
CATGGAGGAT	ACAAATTCAG	TGCTCCAGTT	GTGCCAAGTT	CTTCAATTT	TGGAGGCCCA	480
GCACCAGGGA	TGAATTGAGT	TATCTCTTTC	TTTCTGCTG	TGTGCTTGTA	GTGAAGAGCT	540
TGTGTTCCCT	CTAGTAGTGG	TTCCAGAACT	GGTTCATGTT	ATCTATTCTA	AACTAATAAT	600
CAATAGATGG	ACAAAAGAAA	CAACAACCCC	AGGAGATGGG	ACCTGATCAT	GCAACCTGGC	660
ACTGGAAGAG	AAATCAGCGG	GATTTTGGGG	GTGGGGGGGA	TGGGAGGTAC	CTTAGAGGGA	720
GTATTTTCTT	TATTTTTTGA	AGAAAGTAAG	ATCCTGACTC	TGAAGCTTCA	AAGTGACACT	780
GTGGAAATCT	GAAACGAGGG	GATGTCATGA	AGGCAGCTTT	TCTTTTTCTG	AGGAAAAAAT	840
AGGCATGGGC	TACAGGACTA	TTTAAAATGT	CTCATTTACA	GTATAAAACT	CAAAGGTAGA	900
TGTAATTTTT	ACACCTATGA	GTATTTGTCC	AATTTCTGTC	TCTTCCTCAC	CATTGGGTAT	960
CTATTCTTTA	TATGTAAATA	AGATAAGGTC	ATCTGATAGC	CTTATTCAGT	CTTCATCATT	1020
TTCATCATTG	TTCCATATGA	GATTATTGGA	CATTTATTGT	AGCACTACAT	AACTGATTAT	1080
AAAAATCTGT	AAATGAATTA	GCACTTTCAT	ATTGAAACAA	GCCTGCTAGC	CTATGTATAA	1140
AATAGCAAAA	TGTTTGCTGT	TTATAAAAAG	ATGTAATGGG	GTGGGGGGCA	GGGGTAATTT	1200
CAAGTTATTA	ATTTAAAAAT	GAAC TAGCAA	TTTTGTACCT	GGTGACTTTG	TGGTGCACTC	1260
ACCTCTGATA	GTGACTTGAA	TTCGGTATGT	AAAAAGGGGT	TAGTGGTATT	TCATTGCTGC	1320
TAAAAATGAC	AACTCCCTCT	GTGTCCTGTT	TTTCTTAAAG	CTGTCAGTGT	ACAAGTGGGT	1380
ATTTGAATAC	CAGACCTTAC	TGTAAAAAAT	AAAAAAGGTG	GTATCTAGAG	CATGTAAATT	1440
GGATATAAAG	TTCTGCTCTT	AAAGAGTTGA	TCTAAGAGTA	TGGCTAAACA	TCTATATATG	1500
CAATCTATTA	AAAGAACTTA	ATTCGGCTAT	TATGTCTTGA	TTTGATTGCA	GTTTTTTCCT	1560
AATTATAACA	AATTTTTTCT	CATTGGCCTG	TTTTTAATCC	TGTGCCTAGA	AGGAGTACAA	1620
AATGCACACT	TTACAAAATT	GATATTTAAC	ACTTACCCAC	TCCCCTTTCC	CCATCTCTTC	1680
TACCGCTCTT	GTTGATCGTG	GTATCTGATC	TTGACTAGAT	AGGCTGAAGG	CACATGGTTC	1740
CCTCCAAAAA	CCACTATTGA	TACCACTACA	AAAACAAGCC	AGCAAAAAGA	TACTGTAGAG	1800
AGGTTGGCTT	GCTTCCCTCT	CTTCCTAACT	GCATGTTGAA	AAATAAGCCG	TTATTGATCT	1860
TAAACATCGG	TCAGATGAGT	CATACATTGG	GTTATTTTTT	ATATACATGT	ATACACAAAA	1920
TATTTCAAAT	TGAAAGCAAC	ATCTTAATGG	ATTCAAAAC	ATTACAAGCT	GTTGTCTAAA	1980
ACAGGTGAGA	AAAAAATTTA	TAAC TGTA	AACAAATGCA	CATATTGATA	TTTAAAATGC	2040

GTAATTAAGA AAACCCATTG TTGTTGTGTT TTTCTTGTAT ACCAATAATT AAGCCACTAC2100
 TGTTGGCACT GTTTGGTTTT CTATTTTAACT ACTGAAGGAG TGAAAGTATT TCCTATATTT2160
 ATGAATTTAC TACTAAAATC TTGGCAAAAA AAGAAAAAAA TTGTCTAACG TGTGTGGGTG2220
 AAAACTGTTA ATCAAGTGTT TCTACTCCCC CCCGAAAATC CCCTGAAAGT TGGACACCAA2280
 CTGTATACCC TAGGTTGCTT AAAGGGATTT CACTATTATA TAAAGTCAAT AAAAATGAAG2340
 TAGTTGTATA TATGCAACAT TGTGTACAGA GGGGAAATAA TGAATAGTAT TAAAGAAACA2400
 TTCTCGTCTT CCTTTACCTT TAATCCCCTA ATACCTAGTC TACTTTTTTAA ATTTTCAGAC2460
 TTCACTGCTT TTTGAATTCA TAATTCTAAT TTTCACATTA TTGTTAATGG AAAATCATAT2520
 CTAATAAAGG TTTTAGTTAT TCCCATGCAC AGTATGAAAA TTCTCATTTG CTGAGGTTTT2580
 GTTTCAAGAA AATGTATTGG CATGTCTTTG AGAACATGTT TTATTGTCTC CTGTGTCATA2640
 TAATCCAAAC TAATCTCCGT TTACAGACCT TAACTTGAAA TTAGACCTTA TAATTAAACT2700
 ATTTAAATAG TGTTCAAATG ATAGTTTCTA ATGCATCAAA TATATACCTC AGTTTTCATG2760
 ATTTCCTTTA ACATTATAAT TTGGTATAGA TCAAGAATCT TAACATGTAT CAGTTTCTAG2820
 ATGAGGCTGC AGGATTTTTG GAAAACCTTT TGAATGTATT TACAATATTC TCTTGTAATT2880
 AGCTACATAG GGACTTGTCT TTTTTTCTTT TTACATACAG CTTTTCTTAC AGTTTTATTA2940
 CCCTGTAATT TTTTTTTAGT TGTAGAAGTT AATTCTGATT TTGTGTGGAT TTCAGTATTT3000

GTCTTTTGTTA ATGGCACATA TTAGCATAAA TCACTTTTGT AAATGTAAGC TTTCTTTTTT3060
 TTTCTTGAAA AAGCCTTTCT ATTTATCAGT ATTAAATAAA GGAAGTTAAT CTGTTTCTCT3120
 GCAGGTAATA AAATAGTGAC ACACTGTATT AAGATAGTGA CTGCTATACT CAACTCTGGA3180
 AGAGACTAGA GTATAGAGCA TGAGTGGAAC AACCACAGCC CTTGGGCCAT ATGCTGCTAT3240
 TCAGTCCCAG ATGTAGCCCC TGAAGCAAGC ATAAAGAAAA ATGAATTAAA AATTAAATTA3300
 ATATGGAAAG TTAATAAATG GATTACATTA GTATGACTAA ACCATGTCTT TGGCAAAGAT3360
 CTAACACAAT GTCTTAAGTA TAATAGGTAG TCTCTGTTTG TAAAATAAAT GACTTAAATT3420
 TAAACATCA AAAAAAAAAA 3439

(2) INFORMATION ON SEQ ID NO. 248:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 378 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

SCSSPSCHRG	HERFRIASAC	LDELSCEFL	AGAGGAGAGA	APGPHLPPRG	SVPGDPVRIH	60
ENITESYP	PAIWSVESDD	PNLAAVLRL	VDIKKGNTLL	LQHLKRIISD	LCKLYNLPOH	120
PDVEMLDQPL	PAEQCTQEDV	SSEDEDEEMP	EDTEDLDHYE	MKEEPAEGK	KSEDDGIGKE	180
NLAILEKIKK	NQRQDYLN	VSGSVQATDR	LMKELRDIYR	SQSFKGGNYA	VELVNDSLYD	240
WNVKLLKVDQ	DSALHNDLQI	LKEKEGADFI	LLNFSFKDNF	PFDPFVVRV	SPVLSGGYVL	300
GGGAICMELL	TKQGWSSAYS	IESVIMQISA	TLVKGKARVQ	FGANKSQYSL	TRAQQSYKSL	360
VQIHEKNGWY	TPPKEDG*					378

(2) INFORMATION ON SEQ ID NO. 249:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 281 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

AVGSAALFKD	GGGGTSAAEA	GAAGQRLRSV	NCLAYDEAIM	AQQDRIQQEI	AVQNPLVSER	60
LELSVLYKEY	AEDDNIYQQK	IKDLHKKYSY	IRKTRPDGNC	FYRAFGFSL	EALLDDSKEL	120
QRFKAVSAKS	KEDLVSQGFT	EFTIEDFHNT	FMDLIEQVEK	QTSVADLLAS	FNDQSTSDYL	180
VVYLRLLTSG	YLQRESKFFE	HFIEGGRTVK	EFCQQEVEPM	CKESDHIHII	ALAQALSVSI	240
QVEYMDRGEG	GTTNPHIFPE	GSEPKVYLLY	RPGHYDILYK	*		281

(2) INFORMATION ON SEQ ID NO. 250:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 245 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

DHLQPQKNLC	TCLAPGRGGQ	QGSSGLEPAL	FVEDIVVSRP	VEKVDLGLGA	LREDVRIGGA	60
ALA AVHVLHL	DGHA E GLQR	NDVDV VALLA	HGLHLLLAEL	LDSPSTLDEV	LEELALALQV	120
ARGEQPQVDH	KVVGGALVIE	GGQQVGDRGL	LLHLLNQVHE	RVVEILNCEF	SEALGHQVFL	180
ALGRHSLEPL	QLLAVIQQCL	QVGESESPIE	TVAVRPGLAD	VRVLFVEVLD	LLLIDVVIFS	240
ELLV*						245

(2) INFORMATION ON SEQ ID NO. 251:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 294 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

MLAARLVCLR	TLPSRVFHPA	FTKASPVVKN	SITKNQWLLT	PSREYATKTR	IGIRRGRTGQ	60
ELKEAALEPS	MEKIFKIDQM	GRWFVAGGAA	VGLGALCYYG	LGLSNEIGAI	EKAVIWPQYV	120
KDRIHSTYMY	LAGSIGLTAL	SAIAISRTPV	LMNFM MRGSW	VTIGVTFAAM	VGAGMLVRSI	180
PYDQSPGPKH	LAWLLHSGVM	GAVVAPLTIL	GGPLLIRAAW	YTAGIVGGLS	TVAMCAPSEK	240
FLNMGAPLGV	GLGLVFVSSL	GSMFLPPTTR	GWCHSLLSGN	VRWISSFQHV	PSV*	294

(2) INFORMATION ON SEQ ID NO. 252:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 564 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

MERELNHEKE	RCDQLQAEQK	GLTEVTQSLK	MENEFFKKRF	SDATSKAHQL	EEDIVSVTHK	60
AIEKETELDS	LKDKLKKAQH	EREQLEQCLK	TEKDEKELYK	VHLKNTEIEN	TKLMSEVQTL	120
KNLDGNKESV	ITHFKEEIGR	LQLCLAOKEN	LQRTFLLTTS	SKEDTCFLKE	QLRKAEEQVQ	180
ATRQEVVFLA	KELSDAVNVR	DRTMADLHTA	RENEKVKKQ	LADAVAECLK	NAMKKDQDKT	240
DTLEHELRR	VEDLKLRLQM	AADHYKEKFK	ECQRLQKQIN	KLSDQSANNN	NVFTKKTGNQ	300
QKVNDASVNT	DPATSASTVD	VKPSPSAAEA	DFDIVTKGQV	CEMTKEIADK	TEKYNKCKQL	360
LQDEKAKCNK	YADELAKMEL	KWKEQVKIAE	NVKLELAEVQ	DNYKELKRSL	ENPAERKMED	420
GADGAFYPDE	IQRPPVRVPS	WGLEDNVVCS	QPARNFSPRD	GLEDSSEDSKE	DENVPTAPDP	480
PSQHLRGHGT	GFCFDSSFVD	HKKCPLCELM	FPPNYDQSKF	EEHVESHWKV	CPMCSEQFPP	540
DYDQQVFERH	VQTHFDQNVL	NFD*				564

(2) INFORMATION ON SEQ ID NO. 253:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 250 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

WTGTGRGAVA	IMADPDPRYP	RSSIEDDFNY	GSSVASATVH	IRMAFLRKVY	SILSLQVLLT	60
TVTSTVFLYF	ESVRTFVHES	PALILLFALG	SLGLIFALT	NRHKYPLNLY	LLFGFTLLEA	120
LTVAVVVTFY	DVYIILQAFI	LTFTVFVGLT	VYTLQSKKDF	SKFGAGLFAL	LWILCLSGFL	180
KFFFYSEIME	LVLAAAGALL	FCGFIIYDTH	SLMHKLSPEE	YVLAAISLYL	DIINLFLHLL	240
RFLEAVNKK*						250

(2) INFORMATION ON SEQ ID NO. 254:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 152 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```

PKKGETEREL SASTQTLSHL QGHLPSWPRP APTVTSASRR FIIKKNQKQS QNQNKIQKEK 60
TWGNGMRKRG GEEGRRAGLW MHNSRARGLG RKIPQRPAAC VALARHVVFG GRLPHPVEI 120
LVAGLLGGVK PVSDRQAGKG LGDGGCGRER V* 152

```

(2) INFORMATION ON SEQ ID NO. 255:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 151 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

```

RHAGGGALGN LPPQPPGSGV MHPETCPSTF LASPLPHSIA PGLFLLDFVL VLALFLIFFY 60
YESPGRRGDS GSWPGPGRQV ALEMKGKLCR GAELSLCFSF FPLLLPLHTP VAGRN LGFPE 120
SLGVPPFLPH PGGTPRAPGL FLLLF SFWAV * 151

```

(2) INFORMATION ON SEQ ID NO. 256:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 276 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

GRPGQSPAGA	EEPGPRDSSA	VITQISKEEA	RGPLRGKGDQ	KSAASQKPRS	RGILHSLFCC	60
VCRDDGEALP	AHSGAPLLVE	ENGAIKTPV	QYLLPEAKAQ	DSDKICVVID	LDETLVHSSF	120
KPVNNADFII	PVEIDGVVHQ	VYVLKRPHVD	EFLQRMGELF	ECVLFTASLA	KYADPVADLL	180
DKWGAFRARL	FRESCVFHRG	NYVKDLSRLG	RDLRRVLILD	NSPASYVFHP	DNAVPVASWF	240
DNMSDTELHD	LLPFFEQLSR	VDDVYSVLRQ	PRPGS*			276

(2) INFORMATION ON SEQ ID NO. 257:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 139 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

MFYLAAAVSD	FYVPVSEMPE	HKIQSSGGPL	QITMKMVPKL	LSPLVKDWAP	KAFIISFKLE	60
TDPAIVINRA	RKALEIYQHQ	VVVANILESR	QSFVFIVTKD	SETKLLLSEE	EIEKGVEIEE	120
KIVDNLQSRH	TAFIGDRN*					139

(2) INFORMATION ON SEQ ID NO. 258:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 238 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

PYRQGCPGAA	GQAPGAPPGS	YYPGLPSGTP	GGPYGGAAPG	GPYQPPSS	YGAQQPGLYG	60
QGGAPPNVDP	EAYSWFQSD	SDHSGYISMK	ELKQALVNCN	WSSFNDETC	AMFDKTK	120
SGRIDVYGFS	ALWKFIQQWK	NLFQQYDRDR	SGSISYTELQ	QALSQMGYNL	SPQETQLLVS	180
RYCPRSANPA	MQLDRFIQVC	TQLQVLTEAF	REKDTAVQGN	IRLSFEDFVT	MTASRML*	238

(2) INFORMATION ON SEQ ID NO. 259:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 111 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

TNICLLSGAS	PKVTNGWAQI	NFSFASHRVA	HCGKPELVRT	PVCVFLIHTN	HNKQVCTHLY	60
EPHAKTRHSQ	RSVTRVQQRN	SRFDQNRPC	LLNCQLPLKN	LQKKGHYKNS	*	111

(2) INFORMATION ON SEQ ID NO. 260:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 84 amino acids
 (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

FVKILKFGPL	RIILNEIYRL	TCENIFHRLS	LGLFIRKLFV	CPPVGTFGYL	ILPFQIVKAH	60
RGVFWNHLLS	HFLKSYSIVS	VNI*				84

(2) INFORMATION ON SEQ ID NO. 261:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 197 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

PQTTQCVRR	GLWVNSHIHT	QGRGKHTQVQ	SSQWCRPDLL	SRGCGYGCPSA	SPEQPGQPAP	60
PPRLXQEGEL	CPGEETDRLG	DKTPIAGTCT	AAATAPRTGH	GDGTGREPHC	PLSVCLWFCEP	120
GPAHLEPRQT	GGIEQGPGPD	SPLARCDWKR	LMPGQHQAFC	KSQSQCAESA	STACAVAPQD	180
EVTSTRGGFM	QTHRHC*					197

(2) INFORMATION ON SEQ ID NO. 262:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 191 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

DQLGSGGHFS	LHRLPEQTEE	SSLIVAEPST	SPSAVSVCLH	KPSCPGRDFI	LRSHSTGRAG	60
TFCTLALGLA	EGLVLPWHQP	LPVTSGQRAV	WTWALLNATC	LPGLQVGRTR	TEPQAHTEGA	120
VWLPACPIPM	PRPRGCGCCC	ACPCDGLSVS	QPVSFLPRAE	LPFLXESGRR	CRLSWLLWGS	180
RGTAITPPGQ	*					191

(2) INFORMATION ON SEQ ID NO. 263:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 245 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

UEKMEAFGEA	GWEDFFSTQT	LTFQSILQMK	NADYFSNYVT	EDFTTYINRK	RKNNCHGNHI	60
UEMQAMAEMYN	RPVEVYQYST	EPINTFHGIH	QNEDEPIRVS	YHRNIHNSV	VNPKNKATIGV	120
GLGLPSFKPG	FAEQSLMKNA	IKTSEESWIE	QQMLEDKKRA	TDWEATNEAI	EEQVARESIL	180
QWLRDQEKQA	RQVRGPSQPR	KASATCSSAT	AAASSGLEEW	TSRSPRQGVQ	PRHLSTLSCM	240
LNWA*						245

(2) INFORMATION ON SEQ ID NO. 264:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 221 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

GFRPARCDPV PLPTTRSVAG LPVGRVRQLS RPLLGPDTGS VANIFKGLVI LPEMSLVIRN 60
LQRVIPIRRA PLRSKIEIVR RILGVQKFDL GIICVDNKNI QHINRIYRDR NVPTDVLSP 120

FHEHLKAGEF PQPDFPDDYN LGDIFLGVEY IFHQCKENED YNDVLTVTAT HGLCHLLGFT 180
HGTEAEWQQM FQKEKAVLDE LGRRTGTRLQ ALTRGLFGGS * 221

(2) INFORMATION ON SEQ ID NO. 265:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 109 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

FFFLRSFVIY LCATPAPRSL HPSRVPLSEG TRPSAPSEEA PGQGLQPGPR ASAQLVQHRL 60
LLEHLLPLC LRAVCESQQV TESVGGRRHSQ DVIVIFIFFT LMEDILHS* 109

(2) INFORMATION ON SEQ ID NO. 266:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 372 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

MSFRKVNIII	LVLAVALL	VLHNNFLSLS	SLLRNEVTDS	GIVGPQPIDF	VPNALRHAVD	60
GRQEEIPVVI	AASEDRLGGA	IAAINSIQHN	TRSNVIFYIV	TLNNTADHLR	SWLNSDSLKS	120
IRYKIVNFDP	KLLEGKVKED	PDQGESMKPL	TFARFYLPIL	VPSAKKAIYM	DDDVIVQGDI	180
LALYNTALKP	GHAAAFSEDC	DSASTKVVR	GAGNQYNYIG	YLDYKKERIR	KLSMKASTCS	240
FNPGVFVANL	TEWKRQNITN	QLEKWMKLV	EEGLYSRTLA	GSITTPPLLI	VFYQQHSTID	300
PMWNVRLHGS	SAGKRYSPQF	VKAAKLHWN	GHLKPWGRTA	SYTDVWEKWY	IPDPTGKFNL	360
IRRYTEISNI	K*					372

(2) INFORMATION ON SEQ ID NO. 267:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 73 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

MCLLSQQSPA	ASSLEGAIWR	RAGTQTRALD	AILYHPQQSH	LVGSTALGLT	LPLLYPREPE	60
AGWKDPVAG	GG*					73

(2) INFORMATION ON SEQ ID NO. 268:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 137 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

VPFCPQLREL	CPGVNNQPYL	CESGHCCGET	GCCTYYYELW	WFWLLWTVLI	LFSCCCAFRH	60
RRAKLRLQQQ	QRQVEINLLA	YHGACHGAGP	FPTGSLDLR	FLSTFKPPAY	EDVVHRRPGT	120
SPPLYCGPKA	PLEVVSS					137

(2) INFORMATION ON SEQ ID NO. 269:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 309 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

KHATEQEKTE	EGLGPNVKGI	VTMLMLMLLM	MFAVHCTWVT	SNAYSSPSVV	LASYNHDGTR	60
NILDDFREAY	FWLRQNTDEH	ARVMSWWDYG	YQIAGMANRT	TLVDNNTWNN	SHIALVGKAM	120
SSNETAAYKI	MRTLVDVYVL	VIFGGVIGYS	GDDINKFLWM	VRIAEGEHPK	DIRESDYFTP	180
QGEFRVDKAG	SPTLLNCLMY	KMSYYRFGEM	QLDFRTPPGF	DRTRNAEIGN	KDIKFKHLEE	240
AFTSEHWLVR	IYKVKAPDNR	ETLDHKPRVT	NIFPKQKYL	KKTTKRKRGY	IKNKLVEKKG	300
KKISKKTV*						309

(2) INFORMATION ON SEQ ID NO. 270:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 114 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

IPEDPHIDES	KAKHQAIIMS	TSLRVSPSIH	GYHFDTASRK	KAVGNIFENT	DQESLERLFR	60
NSGDKKAEER	AKIIFAIDQD	VEEKTRALMA	LKKRTKDKLF	QFLKLRKYSI	KVH*	114

(2) INFORMATION ON SEQ ID NO. 271:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

OMQHFAATLQ ASLLSGLQRL ERDRDWKGTR TEQTGYKDSK QFHALCCYRG EQNAFSKDLK 60
 TLPSLQERID ADRAWTDVM RTKENRWLEM TFIQGHFVRP * 101

(2) INFORMATION ON SEQ ID NO. 272:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

PRIPVTLNMK MVMPSQGLD *

21

(2) INFORMATION ON SEQ ID NO. 273:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

CPPVKALIEH	EMKNGIPANR	IVLGGFSQGG	ALSLYTALTC	PHPLAGIVAL	SCWLPLHRAF	60
PQAANGSAKD	LAILQCHGEL	DPMVPVREGA	LTAEKLRVSV	TPARVQFKTY	PGVMHSSCPQ	120
EMAAVKEFLE	KLLPPV*					137

(2) INFORMATION ON SEQ ID NO. 274:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 92 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

MWVLKLDLDRNT	MNVKIPPIFC	SKKKNPKNKK	TNKKPRMFFG	ITEISQTWVF	SYSLCTFFQV	60
LCFACSTDCV	ILIFIDSSLA	MQYPCLTHRC	L*			92

(2) INFORMATION ON SEQ ID NO. 275:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 76 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

ETIADNALPS TEITLESPLL GSFDCLTQDV LCHSEVFIWG RSLYGDVNDS VSGLCITSHW 60
SETPVCQAWI LHCKT* 76

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 120 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

=GGKEKTKKIQ LRNRTMIQHL QKASSISLKK ATDCASAGSE KGWAAGTAAS WVTRQQSQRL 60
 =GVRLRTPLPW EHKRHHWHCKL SVTWPSFLSS ISPNICAHPE ELSGNSRVRA GRRGERTKRE 120

(2) INFORMATION ON SEQ ID NO. 277:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 113 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

VAPFPIPTQE HRGGGEGRLS LSKSSYLHFR RKAETQSRLY INCLADRVTK THWSTCAFSS 60
LCPSLIQTAT CQSPATLKTH GQLPGFTKLT AFLHKVKTIT ASVCGPSATT KLS 113

(2) INFORMATION ON SEQ ID NO. 278:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

PYDPACLLIF SLPLPFLSLS SRSHLPGLKY FVGIAYYIIL ADEPQDNVYT HTHTYTHTKS 60
 QLLKSGLGIR LLCPVKNSCT EVIVT* 86

(2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

NSFKVVKKLA TTWSLSIKRK QGKQTHSLDQ KKLDQVHWNQ SVTTQVTMTS VQEFFTGHR 60
 LIPSPLFNS* 70

(2) INFORMATION ON SEQ ID NO. 280:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 594 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

VSEKCRIDTE	ILPSLFMRCT	TDLNRKDKFP	AITHLKFLAR	DMSEQVLLCA	SSQTSSIVEC	60
WSLRKEGLPV	NNIFQQISPV	VGDKQPTILK	WRILSATNDL	DRVSAVALPK	LPISLTNTDL	120
KVASDTQFYF	GLGLALAFHD	GSVHIVHRLS	LQTMVAFYSS	AAPRPVDEPA	MKRPRTAGPA	180
VHLKAMQLSW	TSLALVGIDS	HGKLSVLRLS	PSMGHPLEV	LALRHLLFLL	EYCMVTGYDW	240
WDILLHVQPS	MVQSLVEKLH	EEYTRQTAAL	QQVLSTRILA	MKASLCKLSP	CTVTRVCDYH	300
TKLFLIAISS	TKSLLRPHF	LNTPDKSPGD	RLTEICTKIT	DVDIDKVMIN	LKTEEFVLDM	360

NTLQALQQLL	QWVGDFVLYL	LASLPNQGSL	LRPGHSFLRD	GTSLGMLREL	MVVIRIWGLL	420
KPSCLPVYTA	TSQTQDSMSL	LFRLLTCLWI	CCRDEGPASE	PDEALVDECC	LLPSQLLIPS	480
LDWLPAADGL	VSRLQPKQPL	RLQFGRAPTL	PGSAATLQLD	GLARAPGQPK	IDHLRRLHLG	540
ACPTTECKAC	TRCGCVTMLK	SPNRTTAVKQ	WEQRWIKNCL	CGGLWWRVPL	SYP*	594

(2) INFORMATION ON SEQ ID NO. 281:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 293 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

LRGTRHQSP	HRQFLIQRC	HCFTAVVLLG	DLSMVTQPHL	VQALHSSVGQ	APRCSLRRWS	60
ILGWPGAL	PSSCRVAALP	GSVGARPNC	RRGCLGCRRL	TRPSLAGSQS	RLGISSWLGS	120
RQHSSTSAS	GSLAGPSSRQ	QIQSLVSRRK	SRDMLSWVSE	VAVYTGRQLG	FRPQMRMTT	180
INSRSMPS	PSRRKLWPG	SREPWLGR	LA SRYSTKSP	TH CKSCCSAC	SV FMSSTNSS	240
RLIMTILSM	ST SVILVQIS	VS RSPGLLSG	V L RKWGRSS	DFR VELMAMRK	SL VW*	293

(2) INFORMATION ON SEQ ID NO. 282:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 173 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

TPALRARSLR DRCARAPCPH GGQQRRRRL NAEGAEGARG GGSSYSEMAE TVADTRRLIT 60
 KPQNLNDAYG PPSNFLEIDV SNPQTVGVGR GRFTTYEIRV KTNLPFIKFK ESTVRRRYS 120
 FEWLRSELER ESKVVVPPLP GKAFRLRQFL EEMMEYLM TI LLRKENKGWS SL* 173

(2) INFORMATION ON SEQ ID NO. 283:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

NYLGRFQPQW FNDNKTTKHG TSNSLIKLLS HLFHRMMRFF LFTVSHQGKK NPPTSCLFFF 60
 LMPGISIHCL FKRPMQKKVD KALAQELGLP VVVPGLPCWG VPKSVP* 107

(2) INFORMATION ON SEQ ID NO. 284:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```

MGNFFFFEPG TCVYAQAGLE LLNSSDPLTS ASQIAETTGT HHCTWLKTIF LKNKSTALHL 60
YLLVSLQFKH TINDYNILFK AGRSGSWLQL EQFITSGLYR ARKIQ 105

```

(2) INFORMATION ON SEQ ID NO. 285:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 119 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```

TGMGGGSGCR ELLCPCKGAE TPVELRKSDG IYRVLGKPWL CLHHGERPWA GSPPSCRSVR 60
LDADGGSDQL ASVSLRHEAA FSSGFQSHSG LPMADRVAKV RNGKCIAYVL PSPTKQIT* 119

```

(2) INFORMATION ON SEQ ID NO. 286:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 110 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

YANQSSSLRF KIKYKLLCFS THSGSIVPEP DCYFFILNII FPHLICLPLI HRHLEKEMGG 60
 CLLSLSLCFV PVVRLAASVA RWAWLEPWVR QVAGGDRERL RGKWWHLLL* 110

(2) INFORMATION ON SEQ ID NO. 287:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 75 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

SQLLGRLRQE NHLNSGGRGC SELRSCHCTP AWATRVKLRL KKKKKEMFFI FFMLSIQALF 60
 HGQQVIFHNV DFPK* 75

(2) INFORMATION ON SEQ ID NO. 288:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 67 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

RRGFLHVGQA GLEFLTSGDP PASATQSAGI TGISHRERPI LLFIYFLRWS LALFRDLRPL 60
 QPSPLQF 67

(2) INFORMATION ON SEQ ID NO. 289:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```

STRPRERRNR SVDECQLINV KXRHXLVCLX CFCLYXQPDV VSXEYKXWGL LPQXLFXISX 60
EKKNDRXXGX IXXARFXST NXXN* 85

```

(2) INFORMATION ON SEQ ID NO. 290:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

MSXXDTXWCV XAVFAFTXNP TVFHXNTNXG XFYPXLSSXL VKKKKMIGXX XEFXGKPXXQ 60
ALXKIXSWXX LTSLPXX* 78

```

(2) INFORMATION ON SEQ ID NO. 291:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 310 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

RAASGRSGSS	VRMSAPRSRP	ASMRWCPAPR	RACTTSTRWT	GPPCATSTSS	ARATRTGPSC	60
RSAGRARSAS	YPPGDVDEIP	DWVHQLVIQK	LVEHRVIPEG	FVNSAVINDY	QPGGCIVSHV	120
DPIHIFERPI	VSVSFFSDSA	LCFGCKFQFK	PIRVSEPVLS	LPVRRGSVTV	LSGYAADEIT	180
HCIRPQDIKE	RRAVIILRKT	RLDAPRLETK	SLSSSVLPPS	YASDRLSGNN	RDPALKPKRS	240
HRKADPDAAH	RPRILEMDKE	ENRRSVLLPT	HRRRGSFSSE	NYWRKSYESS	EDCSEAAGSP	300
ARKVKMRRH*						310

(2) INFORMATION ON SEQ ID NO. 292:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 192 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

SCLPEDDDCS	ALLDVLRPYA	VSDFISSIST	EHSHASPAHR	QGKHWFRHPN	RLELELAAEA	60
QRRVAKEGHG	HDGALEDVDG	VHVGHDAAAG	LVVVDDRAVD	EALGDDAVLH	QLLDHQLMHP	120
VRDLVDVARR	VRGAPGPAPA	SAAGPRTCSP	RRRSTCCAGG	GPPPCARCTG	PSRRGTPPHR	180
CGPRSWSTHP	D*					192

(2) INFORMATION ON SEQ ID NO. 293:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 479 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

MGRCCFYTAG	TLSLLLLVTS	VTLLVARVFQ	KAVDQSIEKK	IVLRNGTEAF	DSWEKPPLPV	60
YTQFYFFNVT	NPEEILRGET	PRVEEVGPYT	YRELRNKANI	QFGDNGTTIS	AVSNKAYVFE	120
RDQSVGDPKI	DLIRTLNIPV	LTVIEWSQVH	FLREIIEAML	KAYQQKLFVT	HTVDELLWGY	180
KDEILSLIHV	FRPDISPYFG	LFYEKNGTND	GDYVFLTGED	SYLNFTKIVE	WNGKTSLDWW	240
ITDKCNMING	TDGDSFHPLI	TKDEVLYVFP	SDFCRSVYIT	FSDYESVQGL	PAFRYKVPAE	300
ILANTSDNAG	FCIPEGNCLG	SGVLNVSICK	NGAPIIMSFP	HFYQADERFV	SAIEGMHPNQ	360
EDHETFDIN	PLTGIILKAA	KRFQINIYVK	KLDDFVETGD	IRTMVFPVMY	LNESVHIDKE	420
TASRLKSMIN	TTLIITNIPY	IIMALGVFFG	LVFTWLACKG	QGSMDEGTAD	ERAPLIRT*	479

(2) INFORMATION ON SEQ ID NO. 294:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 267 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AFLPSPTVAA	QAAAREHAGG	HSAAKNGATG	VELDIEFTSD	GIPVLMHDNT	VDRTTDGTGR	60
LCDLTFEQIR	KLNPAANHRL	RNDFPDEKIP	TLREAVAEC	NHNLTIFFDV	KGHAHKATEA	120
LKKMYMEFPQ	LYNNSVVCSE	LPEVIYKMRQ	TDRDVITALT	HRPWSLSHTG	DGKPRYDTFW	180
KHFIFVMMDI	LLDWSMHNIL	WYLCGISAF	LQKDFVSPAY	LKKWSAKGIQ	VVGWTVNTFD	240
EKSYYESHG	SSYITDSMVE	DCEPHF*				267

(2) INFORMATION ON SEQ ID NO. 295:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 166 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

QILPAFILLF	NGLKRAYACH	AEHETEELGS	DEDDIDEDGQ	EYLEILAKQA	GEDGDDEDWE	60
EDDAEETALE	GYSTIIDDED	NPVDEYQIFK	AIFQTIQNRN	PVWYQALTHG	LNEEQRKQLQ	120
DIATLADQRR	AAHESKMIEK	HGGYKFSAPV	VPSSFNFGGP	APGMN*		166

QILPAFILLF NGLKRAYACH AEHETEELGS DEDDIDEDGQ EYLEILAKQA GEDGDDEDWE 60
EDDAEETALE GYSTIIDDED NPVDEYQIFK AIFQTIQNRN PVWYQALTHG LNEEQRKQLQ 120
DIATLADQRR AAHESKMIEK HGGYKFSAPV VPSSFNFGGP APGMN* 166